GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:51:52 ; Search time 147.68 Seconds
(without alignments)
33.266 Million cell updates/sec

Title: US-09-786-105-4
Perfect score: 20
Sequence: 1 tacggcgtttcgatgaaccc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query Match %	Length	DB	ID	Description
c	1	20	100.0	432	2	US-08-313-185-59	Sequence 59, Appl
c	2	20	100.0	432	3	US-09-082-614A-59	Sequence 59, Appl
c	3	20	100.0	620	2	US-08-757-653-135	Sequence 135, App
c	4	20	100.0	620	2	US-08-757-653-136	Sequence 136, App
c	5	20	100.0	620	2	US-08-757-653-137	Sequence 137, App
	6	20	100.0	620	2	US-08-757-653-138	Sequence 138, App
	7	20	100.0	620	2	US-08-757-653-139	Sequence 139, App
	8	20	100.0	620	2	US-08-757-653-140	Sequence 140, App
c	9	20	100.0	706	4	US-08-797-812-24	Sequence 24, Appl
c	10	20	100.0	970	1	US-08-250-030-1	Sequence 1, Appli
c	11	20	100.0	970	5	PCT-US95-06790-1	Sequence 1, Appli
	12	19	95.0	19	4	US-08-750-088A-71	Sequence 71, Appl
	13	15	75.0	27	1	US-08-250-030-9	Sequence 9, Appli
	14	15	75.0	27	5	PCT-US95-06790-9	Sequence 9, Appli
c	15	14	70.0	3447	2	US-08-313-185-57	Sequence 57, Appl
c	16	14	70.0	3447	3	US-09-082-614A-57	Sequence 57, Appl
	17	13	65.0	383	3	US-08-906-769-169	Sequence 169, App
	18	13	65.0	383	3	US-08-906-616-169	Sequence 169, App
	19	13	65.0	383	3	US-08-639-075A-169	Sequence 169, App
	20	13	65.0	383	4	US-09-012-431-169	Sequence 169, App
	21	13	65.0	383	4	US-09-012-692-169	Sequence 169, App
	22	13	65.0	383	4	US-08-906-613-169	Sequence 169, App
	23	13	65.0	537	3	US-08-906-769-171	Sequence 171, App
	24	13	65.0	537	3	US-08-906-616-171	Sequence 171, App
	25	13	65.0	537	3	US-08-639-075A-171	Sequence 171, App
	26	13	65.0	537	4	US-09-012-431-171	Sequence 171, App
	27	13	65.0	537	4	US-09-012-692-171	Sequence 171, App
	28	13	65.0	537	4	US-08-906-613-171	Sequence 171, App
	29	13	65.0	1938	4	US-09-232-200-29	Sequence 29, Appl
	30	13	65.0	1938	4	US-09-232-197-29	Sequence 29, Appl
	31	13	65.0	1938	4	US-09-232-201-29	Sequence 29, Appl
c	32	13	65.0	3000	2	US-08-896-344A-1	Sequence 1, Appli
c	33	13	65.0	3000	4	US-09-360-682A-1	Sequence 1, Appli
	34	13	65.0	3217	4	US-09-232-200-64	Sequence 64, Appl
	35	13	65.0	3217	4	US-09-232-197-64	Sequence 64, Appl
	36	13	65.0	3217	4	US-09-232-201-64	Sequence 64, Appl
c	37	13	65.0	4403765	4	US-09-103-840A-2	Sequence 2, Appli
	38	12	60.0	391	1	US-08-636-928-6	Sequence 6, Appli
	39	12	60.0	412	4	US-08-976-259-123	Sequence 123, App
c	40	12	60.0	645	1	US-08-459-586-19	Sequence 19, Appl
c	41	12	60.0	645	2	US-08-282-696-19	Sequence 19, Appl
	42	12	60.0	648	5	PCT-US96-04648-4	Sequence 4, Appli
c	43	12	60.0	709	1	US-08-459-586-20	Sequence 20, Appl
c	44	12	60.0	709	2	US-08-282-696-20	Sequence 20, Appl
c	45	12	60.0	728	4	US-08-998-416-615	Sequence 615, App

ALIGNMENTS

RESULT 1
US-08-313-185-59/c
; Sequence 59, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-59

Query Match 100.0%; Score 20; DB 2; Length 432;

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  Best Local Similarity   100.0%;  Pred. No. 0.00054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
           ||||||||||||||||||||
Db     428 TACGGCGTTTCGATGAACCC 409


RESULT   2
US-09-082-614A-59/c
; Sequence 59, Application US/09082614A
; Patent No. 6124098
;  GENERAL INFORMATION:
;    APPLICANT:  Heym, Beate
;    APPLICANT:  Cole, Stewart
;    APPLICANT:  Young, Douglas
;    APPLICANT:  Zhang, Ying
;    APPLICANT:  Honore, Nadine
;    APPLICANT:  Telenti, Amalio
;    APPLICANT:  Bodmer, Thomas
;    TITLE OF INVENTION:  Rapid Detection of Antibiotic Resistance
;    TITLE OF INVENTION:  in Mycobacterium Tuberculosis
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/082,614A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/313,185
;      FILING DATE:  12-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  02356.0068-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-082-614A-59


  Query Match             100.0%;  Score 20;  DB 3;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 0.00054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
           ||||||||||||||||||||
Db     428 TACGGCGTTTCGATGAACCC 409


RESULT   3
US-08-757-653-135/c
; Sequence 135, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  135:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-135


  Query Match             100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity   100.0%;  Pred. No. 0.00054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
           ||||||||||||||||||||
Db     296 TACGGCGTTTCGATGAACCC 277


RESULT   4
US-08-757-653-136/c
; Sequence 136, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
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;       APPLICATION NUMBER:  US/08/757,653
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Ingolia, Diane E.
;       REGISTRATION NUMBER:  40,027
;       REFERENCE/DOCKET NUMBER:  FORS-02565
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 705-8410
;       TELEFAX:  (415) 397-8338
;   INFORMATION FOR SEQ ID NO:  136:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  620 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-757-653-136


  Query Match             100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity   100.0%;  Pred. No. 0.00054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
           ||||||||||||||||||||
Db     296 TACGGCGTTTCGATGAACCC 277


RESULT   5
US-08-757-653-137/c
; Sequence 137, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  137:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-137


  Query Match             100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity   100.0%;  Pred. No. 0.00054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
           ||||||||||||||||||||
Db     296 TACGGCGTTTCGATGAACCC 277


RESULT   6
US-08-757-653-138
; Sequence 138, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  138:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-138


  Query Match             100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity   100.0%;  Pred. No. 0.00054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
           ||||||||||||||||||||
Db     325 TACGGCGTTTCGATGAACCC 344


RESULT   7
US-08-757-653-139
; Sequence 139, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  139:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-139


  Query Match           100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity  100.0%;  Pred. No. 0.00054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
           ||||||||||||||||||||
Db     325 TACGGCGTTTCGATGAACCC 344


RESULT   8
US-08-757-653-140
; Sequence 140, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  140:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-140


  Query Match           100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity  100.0%;  Pred. No. 0.00054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
           ||||||||||||||||||||
Db     325 TACGGCGTTTCGATGAACCC 344


RESULT   9
US-08-797-812-24/c
; Sequence 24, Application US/08797812
; Patent No. 6228575
;  GENERAL INFORMATION:
;    APPLICANT:  Gingeras, Thomas A.
;    APPLICANT:  Mack, David
;    APPLICANT:  Chee, Mark S.
;    APPLICANT:  Berno, Anthony J.
;    APPLICANT:  Stryer, Lubert
;    APPLICANT:  Ghandour, Ghassan
;    APPLICANT:  Wang, Ching
;    TITLE OF INVENTION:  Chip-Based Species Identification and
;    TITLE OF INVENTION:  Phenotypic Characterization of Microorganisms
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/797,812
;      FILING DATE:  07-FEB-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/017,765
;      FILING DATE:  15-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/629,031
;      FILING DATE:  08-APR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/012,631
;      FILING DATE:  01-MAR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,339
;      FILING DATE:  08-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitts, Renee A.
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16528X-018550
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  24:
```

130:219116

TI Method of selecting PCR primer pairs to amplify a group of related nucleotide sequences

IN McClelland, Michael; Pesole, Graziano

PA Sidney Kimmel Cancer Center, USA

SO PCT Int. Appl., 92 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9911823	A2	19990311	WO 1998-US18392	19980904
WO 9911823	A3	19990610		

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

AU 9893027	A1	19990322	AU 1998-93027	19980904
EP 1007739	A2	20000614	EP 1998-945882	19980904

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI

PRAI US 1997-925816	A	19970905	
WO 1998-US18392	W	19980904	

AB The present invention provides a method of detg. a set of primer pairs for amplifying a group of related nucleotide sequences. A method of the invention is performed by identifying a group of related nucleotide sequences; generating the set of primers that matches each of the related nucleotide sequences; detg. for each systematic pairing of each primer which of the related nucleotide sequences are amplified; and selecting from the systematic pairings a subset which amplifies all of the related nucleotide sequences. The invention also provides a method of using a set of primer pairs, which amplify a group of related nucleotide sequences, to identify nucleotide sequences related to the original group of nucleotide sequences. Eight-mer primer pairs are provided for amplification of genes encoding nuclear receptors, G-protein coupled receptors, apoptosis-assocd. proteins, DNA repair enzymes, and replication enzymes. The invention also provides a computer app. for carrying out the computer-executed steps of the method. The invention further provides a computer program product comprising a signal bearing media for carrying out the method.

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;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  706 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-797-812-24


  Query Match             100.0%;  Score 20;  DB 4;  Length 706;
  Best Local Similarity   100.0%;  Pred. No. 0.00053;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    332 TACGGCGTTTCGATGAACCC 313


RESULT  10
US-08-250-030-1/c
; Sequence 1, Application US/08250030
; Patent No. 5643723
;  GENERAL INFORMATION:
;     APPLICANT:  Persing, David H.
;     TITLE OF INVENTION:  Detection of a Genetic Locus Encoding
;     TITLE OF INVENTION:  Resistance to Rifampin in Mycobacterial Cultures and in
;     TITLE OF INVENTION:  Clinical Specimens
;     NUMBER OF SEQUENCES:  15
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Schwegman, Lundberg & Woessner
;       STREET:  3500 IDS Center
;       CITY:  Minneapolis
;       STATE:  MN
;       COUNTRY:  USA
;       ZIP:  55402
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/250,030
;       FILING DATE:  26-MAY-1994
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Mueting, Ann M.
;       REGISTRATION NUMBER:  33,977
;       REFERENCE/DOCKET NUMBER:  150.105US1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  612-339-0331
;       TELEFAX:  612-339-3061
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  970 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA
US-08-250-030-1


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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    671 TACGGCGTTTCGATGAACCC 652


RESULT  11
PCT-US95-06790-1/c
; Sequence 1, Application PC/TUS9506790
;  GENERAL INFORMATION:
;     APPLICANT:  Mayo Foundation for Medical Education and Research
;     APPLICANT:  and Hoffmann-La Roche Inc.
;     TITLE OF INVENTION:  Detection of a Genetic Locus Encoding
;     TITLE OF INVENTION:  Resistance to Rifampin
;     NUMBER OF SEQUENCES:  15
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Schwegman, Lundberg & Woessner
;       STREET:  3500 IDS Center
;       CITY:  Minneapolis
;       STATE:  MN
;       COUNTRY:  USA
;       ZIP:  55402
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/06790
;       FILING DATE:  26-MAY-1995
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Raasch, Kevin W.
;       REGISTRATION NUMBER:  35,651
;       REFERENCE/DOCKET NUMBER:  150.105WO1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  612-339-0331
;       TELEFAX:  612-339-3061
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  970 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA
PCT-US95-06790-1


  Query Match             100.0%;  Score 20;  DB 5;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 0.00053;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    671 TACGGCGTTTCGATGAACCC 652


RESULT  12
US-08-750-088A-71
; Sequence 71, Application US/08750088A
; Patent No. 6329138
;  GENERAL INFORMATION:
;     APPLICANT:  DE BEENHOUWER, HANS
;     APPLICANT:  PORTAELS, FRAN OISE
;     APPLICANT:  MACHTELINCKX, LIEVE
;     APPLICANT:  JANNES, GEERT
;     APPLICANT:  ROSSAU, RUDI
;     TITLE OF INVENTION:  METHOD FOR DETECTION OF THE ANTIBIOTIC
;     TITLE OF INVENTION:  RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
;     NUMBER OF SEQUENCES:  71
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;       STREET:  1100 NEW YORK AVENUE, SUITE 600
;       CITY:  WASHINGTON
;       STATE:  D.C.
;       COUNTRY:  US
;       ZIP:  20005-3934
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/750,088A
;      FILING DATE:  21-FEB-1997
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GOLDSTEIN, JORGE A.
;      REGISTRATION NUMBER:  29,021
;      REFERENCE/DOCKET NUMBER:  1657.0010000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-750-088A-71


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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      1 TACGGCGTTTCGATGAACC 19


RESULT  13
US-08-250-030-9
; Sequence 9, Application US/08250030
; Patent No. 5643723
;  GENERAL INFORMATION:
;    APPLICANT:  Persing, David H.
;    TITLE OF INVENTION:  Detection of a Genetic Locus Encoding
;    TITLE OF INVENTION:  Resistance to Rifampin in Mycobacterial Cultures and in
;    TITLE OF INVENTION:  Clinical Specimens
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schwegman, Lundberg & Woessner
;      STREET:  3500 IDS Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/250,030
;      FILING DATE:  26-MAY-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueting, Ann M.
;      REGISTRATION NUMBER:  33,977
;      REFERENCE/DOCKET NUMBER:  150.105US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-339-0331
;      TELEFAX:  612-339-3061
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-250-030-9


  Query Match             75.0%;  Score 15;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.7;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 cgtttcgatgaaccc 20
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Db      1 CGTTTCGATGAACCC 15


RESULT  14
PCT-US95-06790-9
; Sequence 9, Application PC/TUS9506790
;  GENERAL INFORMATION:
;    APPLICANT:  Mayo Foundation for Medical Education and Research
;    APPLICANT:  and Hoffmann-La Roche Inc.
;    TITLE OF INVENTION:  Detection of a Genetic Locus Encoding
;    TITLE OF INVENTION:  Resistance to Rifampin
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schwegman, Lundberg & Woessner
;      STREET:  3500 IDS Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/06790
;      FILING DATE:  26-MAY-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Raasch, Kevin W.
;      REGISTRATION NUMBER:  35,651
;      REFERENCE/DOCKET NUMBER:  150.105WO1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-339-0331
;      TELEFAX:  612-339-3061
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
PCT-US95-06790-9


  Query Match             75.0%;  Score 15;  DB 5;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.7;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 cgtttcgatgaaccc 20
          |||||||||||||||
Db      1 CGTTTCGATGAACCC 15


RESULT  15
US-08-313-185-57/c
; Sequence 57, Application US/08313185
; Patent No. 5851763
;  GENERAL INFORMATION:
;    APPLICANT:  Heym, Beate
;    APPLICANT:  Cole, Stewart
;    APPLICANT:  Young, Douglas
;    APPLICANT:  Zhang, Ying
;    APPLICANT:  Honore, Nadine
;    APPLICANT:  Telenti, Amalio
;    APPLICANT:  Bodmer, Thomas
;    TITLE OF INVENTION:  Rapid Detection of Antibiotic Resistance
```

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;    TITLE OF INVENTION:  in Mycobacterium Tuberculosis
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/313,185
;      FILING DATE:  12-OCT-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  02356.0068-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3447 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-313-185-57


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  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db    1448 GTTTCGATGAACCC 1435


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Job time: 7180 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:54:31 ; Search time 562.71 Seconds
(without alignments)
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Title: US-09-786-105-1
Perfect score: 20
Sequence: 1 tacggtcggcgagctgatcc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

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Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	17	AAT12092	M. tuberculosis rp
2	20	100.0	20	21	AAA49823	Mycobacterium tube
3	20	100.0	20	21	AAA49825	Mycobacterium tube
4	20	100.0	306	19	AAX27214	RpoB gene fragment
5	20	100.0	306	19	AAX27175	RpoB gene fragment
6	20	100.0	306	19	AAX27179	RpoB gene fragment
7	20	100.0	306	19	AAX27180	RpoB gene fragment
8	20	100.0	306	24	AAS99526	Mycobacterium spec
9	20	100.0	306	24	AAS99527	Mycobacterium spec
10	20	100.0	306	24	AAS99530	Mycobacterium spec
11	20	100.0	306	24	AAS99531	Mycobacterium spec
12	20	100.0	432	14	AAQ61457	M.tuberculosis rpo
13	20	100.0	480	21	AAA49863	Mycobacterium tube
14	20	100.0	970	17	AAT09676	Mycobacterium tube
15	20	100.0	3519	22	AAH51976	Mycobacterium tube
16	20	100.0	3534	22	AAH02079	Mycobacterium tube
17	20	100.0	3853	21	AAA74651	Mycobacterium tube
18	20	100.0	3853	21	AAA89994	M. tuberculosis rp
19	19	95.0	306	19	AAX27217	RpoB gene fragment
20	19	95.0	306	24	AAS99551	Mycobacterium spec
21	19	95.0	21500	23	AAS59633	Propionibacterium
22	18	90.0	25	17	AAT12091	M. tuberculosis rp
c 23	18	90.0	87	22	AAC88922	Mycobacterium tube
24	16	80.0	306	19	AAX27212	RpoB gene fragment
25	16	80.0	306	19	AAX27218	RpoB gene fragment
26	16	80.0	306	19	AAX27193	RpoB gene fragment
27	16	80.0	306	19	AAX27196	RpoB gene fragment
28	16	80.0	306	19	AAX27204	RpoB gene fragment
29	16	80.0	306	19	AAX27177	RpoB gene fragment
30	16	80.0	306	19	AAX27182	RpoB gene fragment
31	16	80.0	306	19	AAX27183	RpoB gene fragment
32	16	80.0	306	19	AAX27186	RpoB gene fragment
33	16	80.0	306	24	AAS99539	Mycobacterium spec
34	16	80.0	306	24	AAS99557	Mycobacterium spec
35	16	80.0	306	24	AAS99560	Mycobacterium spec
36	16	80.0	306	24	AAS99565	Mycobacterium spec
37	16	80.0	306	24	AAS99568	Mycobacterium spec
38	16	80.0	27426	23	AAS59541	Propionibacterium
39	15	75.0	1092	22	AAS02316	B. subtilis DNA en
40	15	75.0	2488	23	ABL14021	Drosophila melanog
41	15	75.0	2772	23	AAS54170	Pseudomonas aerugi
c 42	15	75.0	4544	23	ABL14020	Drosophila melanog
43	15	75.0	4403765	22	AAI99683	Mycobacterium tube
44	15	75.0	4411529	22	AAI99682	Mycobacterium tube
45	14	70.0	50	19	AAV31045	Expression vector

ALIGNMENTS

RESULT 1
AAT12092
ID AAT12092 standard; DNA; 20 BP.
XX
AC AAT12092;
XX
DT 10-JUL-1996 (first entry)
XX
DE M. tuberculosis rpoB gene fragment amplification primer P2.
XX
KW Antibiotic; resistance; spectrum; gene; mycobacterium;
KW determination; amplification; tuberculosis; rpoB; fragment;
KW primer; differential; hybridisation; pattern; rifampicin;
KW rifabutin; species identification; ss.
XX
OS Synthetic.
XX
PN WO9533851-A2.
XX
PD 14-DEC-1995.
XX
PF 09-JUN-1995; 95WO-EP02230.
XX
PR 09-JUN-1994; 94EP-0870093.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI De Beenhouwer H, Jannes G, Machtelinckx L, Portaels F;
PI Rossau R;
XX
DR WPI; 1996-040250/04.
XX

PT Probes and primers for determn. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene
XX
PS Claim 22; Page 39; 69pp; English.
XX
CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT12091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrids formed and
CC inferring the ARS, and opt. the spp., from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampicin and/or rifabutin resistance in M. leprae
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determn.
CC of ARS and spp. identity.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 1 tacggtcggcgagctgatcc 20

RESULT 2
AAA49823
ID AAA49823 standard; DNA; 20 BP.
XX
AC AAA49823;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene amplification primer rpoB-F.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 4; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene amplification primer rpoB-F (bp
CC 2201-2220). It is used with the reverse primer given in AAA49824
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 1 tacggtcggcgagctgatcc 20

RESULT 3
AAA49825
ID AAA49825 standard; DNA; 20 BP.
XX
AC AAA49825;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-5s.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene sequencing primer rpoB-5s (bp
CC 2201-2220). It is used with the reverse primer given in AAA49826 and
CC with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.

CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 1 tacggtcggcgagctgatcc 20

RESULT 4
AAX27214
ID AAX27214 standard; DNA; 306 BP.
XX
AC AAX27214;
XX
DT 27-MAY-1999 (first entry)
XX
DE RpoB gene fragment.
XX
KW RpoB gene; mycobacteria; phylogenetic tree construction;
KW mycobacterial species identification; phylogenetic analysis; ss.
XX
OS Mycobacteria tuberculosis.
XX
PN WO9905316-A1.
XX
PD 04-FEB-1999.
XX
PF 28-JUL-1998; 98KR-0000228.
XX
PR 28-JUL-1997; 97KR-0035501.
XX
PA (BION-) BIONEER CORP.
XX
PI Kim B, Kook Y;
XX
DR WPI; 1998-539367/46.
XX
PT New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the rpoB gene from mycobacterial
PT species, useful for detecting and identifying mycobacterial species
XX
PS Claim 43; Page 75-76; 91pp; English.
XX
CC This sequence represents a mycobacterial rpoB gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the rpoB gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterising these species. In addition to
CC phylogenetic analysis, the rpoB gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in M. tuberculosis.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 5
AAX27175
ID AAX27175 standard; DNA; 306 BP.
XX
AC AAX27175;
XX
DT 27-MAY-1999 (first entry)
XX
DE RpoB gene fragment.
XX
KW RpoB gene; mycobacteria; phylogenetic tree construction;
KW mycobacterial species identification; phylogenetic analysis; ss.
XX
OS Mycobacteria africanum.
XX
PN WO9905316-A1.
XX
PD 04-FEB-1999.
XX
PF 28-JUL-1998; 98KR-0000228.
XX
PR 28-JUL-1997; 97KR-0035501.
XX
PA (BION-) BIONEER CORP.
XX
PI Kim B, Kook Y;
XX
DR WPI; 1998-539367/46.
XX
PT New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the rpoB gene from mycobacterial
PT species, useful for detecting and identifying mycobacterial species
XX
PS Claim 4; Page 62-63; 91pp; English.
XX
CC This sequence represents a mycobacterial rpoB gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the rpoB gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterising these species. In addition to
CC phylogenetic analysis, the rpoB gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in M. tuberculosis.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 6
AAX27179

ID AAX27179 standard; DNA; 306 BP.
XX
AC AAX27179;
XX
DT 27-MAY-1999 (first entry)
XX
DE RpoB gene fragment.
XX
KW RpoB gene; mycobacteria; phylogenetic tree construction;
KW mycobacterial species identification; phylogenetic analysis; ss.
XX
OS Mycobacteria bovis.
XX
PN WO9905316-A1.
XX
PD 04-FEB-1999.
XX
PF 28-JUL-1998; 98KR-0000228.
XX
PR 28-JUL-1997; 97KR-0035501.
XX
PA (BION-) BIONEER CORP.
XX
PI Kim B, Kook Y;
XX
DR WPI; 1998-539367/46.
XX
PT New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the rpoB gene from mycobacterial
PT species, useful for detecting and identifying mycobacterial species
XX
PS Claim 8; Page 64; 91pp; English.
XX
CC This sequence represents a mycobacterial rpoB gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the rpoB gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterising these species. In addition to
CC phylogenetic analysis, the rpoB gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in M. tuberculosis.
XX
SQ Sequence 306 BP; 56 A; 96 C; 107 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 7
AAX27180
ID AAX27180 standard; DNA; 306 BP.
XX
AC AAX27180;
XX
DT 27-MAY-1999 (first entry)
XX
DE RpoB gene fragment.
XX
KW RpoB gene; mycobacteria; phylogenetic tree construction;
KW mycobacterial species identification; phylogenetic analysis; ss.
XX
OS Mycobacteria bovis.
XX
PN WO9905316-A1.
XX
PD 04-FEB-1999.
XX
PF 28-JUL-1998; 98KR-0000228.
XX
PR 28-JUL-1997; 97KR-0035501.
XX
PA (BION-) BIONEER CORP.
XX
PI Kim B, Kook Y;
XX
DR WPI; 1998-539367/46.
XX
PT New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the rpoB gene from mycobacterial
PT species, useful for detecting and identifying mycobacterial species
XX
PS Claim 9; Page 64; 91pp; English.
XX
CC This sequence represents a mycobacterial rpoB gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the rpoB gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterising these species. In addition to
CC phylogenetic analysis, the rpoB gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in M. tuberculosis.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 8
AAS99526
ID AAS99526 standard; DNA; 306 BP.
XX
AC AAS99526;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #1.
XX
KW Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200192573-A1.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-KR00904.
XX
PR 30-MAY-2000; 2000KR-0029369.
XX
PA (BIOM-) BIOMEDLAB CO LTD.
XX
PI Kim H, Kim N, Yoon S, Kim J, Park M;
XX

DR WPI; 2002-075472/10.
XX
PT Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -
XX
PS Disclosure; Page 21; 74pp; English.
XX
CC The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 9
AAS99527
ID AAS99527 standard; DNA; 306 BP.
XX
AC AAS99527;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #2.
XX
KW Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
OS Mycobacterium africanum.
XX
PN WO200192573-A1.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-KR00904.
XX
PR 30-MAY-2000; 2000KR-0029369.
XX
PA (BIOM-) BIOMEDLAB CO LTD.
XX
PI Kim H, Kim N, Yoon S, Kim J, Park M;
XX
DR WPI; 2002-075472/10.
XX
PT Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -
XX
PS Disclosure; Page 21; 74pp; English.
XX
CC The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 10
AAS99530
ID AAS99530 standard; DNA; 306 BP.
XX
AC AAS99530;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #5.
XX
KW Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
OS Mycobacterium bovis.
XX
PN WO200192573-A1.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-KR00904.
XX
PR 30-MAY-2000; 2000KR-0029369.
XX
PA (BIOM-) BIOMEDLAB CO LTD.
XX
PI Kim H, Kim N, Yoon S, Kim J, Park M;
XX
DR WPI; 2002-075472/10.
XX
PT Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -
XX
PS Disclosure; Page 21; 74pp; English.
XX
CC The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of

CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 11
AAS99531
ID AAS99531 standard; DNA; 306 BP.
XX
AC AAS99531;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #6.
XX
KW Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
OS Mycobacterium bovis.
XX
PN WO200192573-A1.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-KR00904.
XX
PR 30-MAY-2000; 2000KR-0029369.
XX
PA (BIOM-) BIOMEDLAB CO LTD.
XX
PI Kim H, Kim N, Yoon S, Kim J, Park M;
XX
DR WPI; 2002-075472/10.
XX
PT Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -
XX
PS Disclosure; Page 21; 74pp; English.
XX
CC The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 12
AAQ61457
ID AAQ61457 standard; DNA; 432 BP.
XX
AC AAQ61457;
XX
DT 17-MAY-1994 (first entry)
XX
DE M.tuberculosis rpoB gene fragment.
XX
KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KW mutant; ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9322454-A.
XX
PD 11-NOV-1993.
XX
PF 30-APR-1993; 93WO-EP01063.
XX
PR 17-SEP-1992; 92FR-0011098.
PR 30-APR-1992; 92US-0875940.
PR 14-AUG-1992; 92US-0929206.
PR 16-APR-1993; 93FR-0004545.
XX
PA (ASSI-) ASSISTANCE PUBLIQUE.
PA (INSP) INST PASTEUR.
PA (MEDI-) MEDICAL RES COUNCIL.
PA (UYBE-) UNIV BERNE.
PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
PI Young D, Zhang Y;
XX
DR WPI; 1993-368812/46.
DR P-PSDB; AAR51372.
XX
PT Rapid detection of antibiotic resistance in Mycobacteria - esp.
PT isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in katG, rpoB or rpsL genes
XX
PS Example 2; Fig 13; 97pp; English.
XX
CC PCR amplification was used to obtain rpoB genes from rifampicin-
CC resistant Mycobacterium leprae strains. A comparison with the
CC sequence of the rpoB gene from sensitive strains (AAQ51532) revealed
CC mutations in the region encoding amino acids 400-450. The corresp.
CC region was isolated from M.tuberculosis (AAQ61457). A common
CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
SQ Sequence 432 BP; 78 A; 139 C; 148 G; 67 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20

```
                    ||||||||||||||||||||
Db      18 tacggtcggcgagctgatcc 37


RESULT 13
AAA49863
ID   AAA49863 standard; DNA; 480 BP.
XX
AC   AAA49863;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Mycobacterium tuberculosis rpoB gene (rifampin resistance).
XX
KW   Antibiotic resistance; rpoB gene; rifampin resistance; ss.
XX
OS   Mycobacterium tuberculosis.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     complement(41..60)
FT                   /*tag=  a
FT                   /note= "primer of AAA49823"
FT   primer_bind     372..391
FT                   /*tag=  b
FT                   /note= "primer of AAA49824"
XX
PN   WO200036142-A1.
XX
PD   22-JUN-2000.
XX
PF   10-DEC-1999;   99WO-CA01177.
XX
PR   11-DEC-1998;   98US-0111794.
XX
PA   (VISI-) VISIBLE GENETICS INC.
XX
PI   Shipman R;
XX
DR   WPI; 2000-431611/37.
XX
PT   Method for the detection and characterization of Mycobacterium
PT   tuberculosis with antibiotic resistance in a sample -
XX
PS   Disclosure; Page 5; 43pp; English.
XX
CC   The present sequence is that of the Mycobacterium tuberculosis
CC   rpoB (rifampin resistance) gene (bp2161-2640).  Amplification and
CC   cycle sequencing primers (see AAA49823-62) are used for the detection
CC   and analysis of antibiotic resistance-associated mutations in
CC   defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC   (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC   (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC   (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC   These primers can be used in a method for the detection and
CC   characterization of M. tuberculosis present in a sputum sample.
CC   The method involves performing a sequencing procedure, with or
CC   without prior amplification, to detect the presence of M.
CC   tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC   and 23S genes for the presence of antibiotic-inducing mutations.
CC   If M. tuberculosis is detected, a second sequencing procedure is
CC   performed on the sample to evaluate additional genes for the
CC   presence of antibiotic resistance-inducing mutations.  Genotypic
CC   tests are rapid, sensitive and accurate providing information as to
CC   antibiotic treatment options.
XX
SQ   Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 21;  Length 480;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggtcggcgagctgatcc 20
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                    ||||||||||||||||||||
Db      41 tacggtcggcgagctgatcc 60


RESULT 14
AAT09676
ID   AAT09676 standard; DNA; 970 BP.
XX
AC   AAT09676;
XX
DT   15-OCT-1996  (first entry)
XX
DE   Mycobacterium tuberculosis rpoB gene DNA sequence.
XX
KW   Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;
KW   polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.
XX
OS   Mycobacterium tuberculosis.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     10..27
FT                   /*tag=  a
FT                   /note= "primer FENLFF"
FT   primer_bind     226..243
FT                   /*tag=  b
FT                   /note= "primer DDIDHL"
FT   primer_bind     226..240
FT                   /*tag=  c
FT                   /note= "primer DDIDH"
FT   primer_bind     338..364
FT                   /*tag=  d
FT                   /note= "primer rpo95"
FT   primer_bind     348..373
FT                   /*tag=  e
FT                   /note= "primer rpo105"
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FT                   /note= "primer rpo293"
FT   primer_bind     640..666
FT                   /*tag=  r
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PN   WO9533074-A1.
XX
PD   07-DEC-1995.
XX
PF   26-MAY-1995;   95WO-US06790.
XX
PR   26-MAY-1994;   94US-0250030.
XX
PA   (HOFF ) HOFFMANN LA ROCHE INC.
PA   (MAYO-) MAYO FOUNDATION.
XX
PI   Felmlee TA,  Hunt JM,  Persing DH,  Roberts GD,  Whelen AC;
PI   Young KKY;
XX
DR   WPI; 1996-030581/03.
XX
PT   Detection of Mycobacterium tuberculosis - by amplifying sample DNA
PT   with a primer set that targets portions of the gene encoding rpoB.
XX
PS   Disclosure; Fig.3; 54pp; English.
XX
CC   This oligonucleotide DNA primer is specific for Mycobacterium
CC   tuberculosis, and may be used to amplify a sample DNA by targeting
CC   a portion of the gene encoding rpoB.  The 1st several bases comprise a
CC   nonhybridizing tail consisting of filler bases followed by
CC   a restriction site incorporated to facilitate cloning using the
CC   amplicon at a later date, if desired.  The remaining bases hybridize
CC   to bacterial rpoB DNA.  The method provides for the detection of M.
CC   tuberculosis and the concurrent determination of its drug
CC   susceptibility, particularly to rifamycin.  The method can provide
CC   often greater than 95% sensitivity and 100% specificity.  The
CC   biological sample is a fluid or tissue sample from a human.
XX
SQ   Sequence 970 BP; 182 A; 302 C; 330 G; 156 T; 0 other;


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  Best Local Similarity   100.0%;  Pred. No. 0.023;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db    261 tacggtcggcgagctgatcc 280


RESULT  15
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ID   AAH51976 standard; DNA; 3519 BP.
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AC   AAH51976;
XX
DT   04-SEP-2001  (first entry)
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DE   Mycobacterium tuberculosis potential drug target gene SEQ ID 30.
XX
KW   Drug target; growth; organism viability; characterisation; ds.
XX
OS   Mycobacterium tuberculosis.
XX
PN   WO200135317-A1.
XX
PD   17-MAY-2001.
XX
PF   13-NOV-2000; 2000WO-US31152.
XX
PR   12-NOV-1999;   99US-0165086.
PR   12-NOV-1999;   99US-0165124.
PR   01-FEB-2000; 2000US-0179531.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Eisenberg D,  Rotstein SH,  Marcotte EM;
XX
DR   WPI; 2001-329193/34.
DR   P-PSDB; AAG81125.
XX
PT   Identifying nucleotide or polypeptide sequence for use as drug target,
PT   involves providing algorithm that analyzes a functional relationship
PT   between nucleotide or polypeptide sequences, and comparing the
PT   sequences -
XX
PS   Disclosure; Page 68-69; 207pp; English.
XX
CC   This invention relates to a method for identifying a nucleotide or
CC   polypeptide sequence that may be a drug target, or essential for growth
CC   or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
CC   represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
CC   tuberculosis proteins which are potential drug targets. The DNA and
CC   protein sequences are used to illustrate the method of the invention. The
CC   method involves providing an unknown nucleotide or polypeptide sequences,
CC   and comparing it to a number of sequences along with at least one
CC   algorithm capable of analysing a functional relationship between
CC   nucleotide and polypeptide sequences. The method is useful for
CC   characterising the function of nucleic acids and polypeptides that may be
CC   useful as a target for a drug or essential for the growth or viability of
CC   an organism.
XX
SQ   Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 22;  Length 3519;
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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          ||||||||||||||||||||
Db   1119 tacggtcggcgagctgatcc 1138


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Job time: 7610 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:51:45 ; Search time 147.68 Seconds
(without alignments)
33.266 Million cell updates/sec

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Perfect score: 20
Sequence: 1 tacggcgtttcgatgaaccc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	20	100.0	432	2	US-08-313-185-59	Sequence 59, Appl
c	2	20	100.0	432	3	US-09-082-614A-59	Sequence 59, Appl
c	3	20	100.0	620	2	US-08-757-653-135	Sequence 135, App
c	4	20	100.0	620	2	US-08-757-653-136	Sequence 136, App
c	5	20	100.0	620	2	US-08-757-653-137	Sequence 137, App
	6	20	100.0	620	2	US-08-757-653-138	Sequence 138, App
	7	20	100.0	620	2	US-08-757-653-139	Sequence 139, App
	8	20	100.0	620	2	US-08-757-653-140	Sequence 140, App
c	9	20	100.0	706	4	US-08-797-812-24	Sequence 24, Appl
c	10	20	100.0	970	1	US-08-250-030-1	Sequence 1, Appli
c	11	20	100.0	970	5	PCT-US95-06790-1	Sequence 1, Appli
	12	19	95.0	19	4	US-08-750-088A-71	Sequence 71, Appl
	13	15	75.0	27	1	US-08-250-030-9	Sequence 9, Appli
	14	15	75.0	27	5	PCT-US95-06790-9	Sequence 9, Appli
c	15	14	70.0	3447	2	US-08-313-185-57	Sequence 57, Appl
c	16	14	70.0	3447	3	US-09-082-614A-57	Sequence 57, Appl
	17	13	65.0	383	3	US-08-906-769-169	Sequence 169, App
	18	13	65.0	383	3	US-08-906-616-169	Sequence 169, App
	19	13	65.0	383	3	US-08-639-075A-169	Sequence 169, App
	20	13	65.0	383	4	US-09-012-431-169	Sequence 169, App
	21	13	65.0	383	4	US-09-012-692-169	Sequence 169, App
	22	13	65.0	383	4	US-08-906-613-169	Sequence 169, App
	23	13	65.0	537	3	US-08-906-769-171	Sequence 171, App
	24	13	65.0	537	3	US-08-906-616-171	Sequence 171, App
	25	13	65.0	537	3	US-08-639-075A-171	Sequence 171, App
	26	13	65.0	537	4	US-09-012-431-171	Sequence 171, App
	27	13	65.0	537	4	US-09-012-692-171	Sequence 171, App
	28	13	65.0	537	4	US-08-906-613-171	Sequence 171, App
	29	13	65.0	1938	4	US-09-232-200-29	Sequence 29, Appl
	30	13	65.0	1938	4	US-09-232-197-29	Sequence 29, Appl
	31	13	65.0	1938	4	US-09-232-201-29	Sequence 29, Appl
c	32	13	65.0	3000	2	US-08-896-344A-1	Sequence 1, Appli
c	33	13	65.0	3000	4	US-09-360-682A-1	Sequence 1, Appli
	34	13	65.0	3217	4	US-09-232-200-64	Sequence 64, Appl
	35	13	65.0	3217	4	US-09-232-197-64	Sequence 64, Appl
	36	13	65.0	3217	4	US-09-232-201-64	Sequence 64, Appl
c	37	13	65.0	4403765	4	US-09-103-840A-2	Sequence 2, Appli
	38	12	60.0	391	1	US-08-636-928-6	Sequence 6, Appli
	39	12	60.0	412	4	US-08-976-259-123	Sequence 123, App
c	40	12	60.0	645	1	US-08-459-586-19	Sequence 19, Appl
c	41	12	60.0	645	2	US-08-282-696-19	Sequence 19, Appl
	42	12	60.0	648	5	PCT-US96-04648-4	Sequence 4, Appli
c	43	12	60.0	709	1	US-08-459-586-20	Sequence 20, Appl
c	44	12	60.0	709	2	US-08-282-696-20	Sequence 20, Appl
c	45	12	60.0	728	4	US-08-998-416-615	Sequence 615, App

ALIGNMENTS

RESULT 1
US-08-313-185-59/c
; Sequence 59, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-59

Query Match 100.0%; Score 20; DB 2; Length 432;

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  Best Local Similarity   100.0%;  Pred. No. 0.00054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
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Db     428 TACGGCGTTTCGATGAACCC 409


RESULT   2
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; Sequence 59, Application US/09082614A
; Patent No. 6124098
;  GENERAL INFORMATION:
;    APPLICANT:  Heym, Beate
;    APPLICANT:  Cole, Stewart
;    APPLICANT:  Young, Douglas
;    APPLICANT:  Zhang, Ying
;    APPLICANT:  Honore, Nadine
;    APPLICANT:  Telenti, Amalio
;    APPLICANT:  Bodmer, Thomas
;    TITLE OF INVENTION:  Rapid Detection of Antibiotic Resistance
;    TITLE OF INVENTION:  in Mycobacterium Tuberculosis
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/082,614A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/313,185
;      FILING DATE:  12-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  02356.0068-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-082-614A-59


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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
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Db     428 TACGGCGTTTCGATGAACCC 409


RESULT   3
US-08-757-653-135/c
; Sequence 135, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  135:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-135


  Query Match             100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity   100.0%;  Pred. No. 0.00054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
           ||||||||||||||||||||
Db     296 TACGGCGTTTCGATGAACCC 277


RESULT   4
US-08-757-653-136/c
; Sequence 136, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
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;       APPLICATION NUMBER:  US/08/757,653
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Ingolia, Diane E.
;       REGISTRATION NUMBER:  40,027
;       REFERENCE/DOCKET NUMBER:  FORS-02565
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 705-8410
;       TELEFAX:  (415) 397-8338
;   INFORMATION FOR SEQ ID NO:  136:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  620 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-757-653-136


  Query Match           100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity  100.0%;  Pred. No. 0.00054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    296 TACGGCGTTTCGATGAACCC 277


RESULT   5
US-08-757-653-137/c
; Sequence 137, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  137:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-137


  Query Match           100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity  100.0%;  Pred. No. 0.00054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    296 TACGGCGTTTCGATGAACCC 277


RESULT   6
US-08-757-653-138
; Sequence 138, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  138:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-138


  Query Match           100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity  100.0%;  Pred. No. 0.00054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
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Db    325 TACGGCGTTTCGATGAACCC 344


RESULT   7
US-08-757-653-139
; Sequence 139, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
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```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  139:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-139


  Query Match             100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity   100.0%;  Pred. No. 0.00054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    325 TACGGCGTTTCGATGAACCC 344


RESULT   8
US-08-757-653-140
; Sequence 140, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  140:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-140


  Query Match             100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity   100.0%;  Pred. No. 0.00054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    325 TACGGCGTTTCGATGAACCC 344


RESULT   9
US-08-797-812-24/c
; Sequence 24, Application US/08797812
; Patent No. 6228575
;  GENERAL INFORMATION:
;    APPLICANT:  Gingeras, Thomas A.
;    APPLICANT:  Mack, David
;    APPLICANT:  Chee, Mark S.
;    APPLICANT:  Berno, Anthony J.
;    APPLICANT:  Stryer, Lubert
;    APPLICANT:  Ghandour, Ghassan
;    APPLICANT:  Wang, Ching
;    TITLE OF INVENTION:  Chip-Based Species Identification and
;    TITLE OF INVENTION:  Phenotypic Characterization of Microorganisms
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/797,812
;      FILING DATE:  07-FEB-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/017,765
;      FILING DATE:  15-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/629,031
;      FILING DATE:  08-APR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/012,631
;      FILING DATE:  01-MAR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,339
;      FILING DATE:  08-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitts, Renee A.
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16528X-018550
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  24:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  706 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-797-812-24


  Query Match            100.0%;  Score 20;  DB 4;  Length 706;
  Best Local Similarity   100.0%;  Pred. No. 0.00053;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
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Db    332 TACGGCGTTTCGATGAACCC 313


RESULT  10
US-08-250-030-1/c
; Sequence 1, Application US/08250030
; Patent No. 5643723
;  GENERAL INFORMATION:
;    APPLICANT:  Persing, David H.
;    TITLE OF INVENTION:  Detection of a Genetic Locus Encoding
;    TITLE OF INVENTION:  Resistance to Rifampin in Mycobacterial Cultures and in
;    TITLE OF INVENTION:  Clinical Specimens
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schwegman, Lundberg & Woessner
;      STREET:  3500 IDS Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/250,030
;      FILING DATE:  26-MAY-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueting, Ann M.
;      REGISTRATION NUMBER:  33,977
;      REFERENCE/DOCKET NUMBER:  150.105US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-339-0331
;      TELEFAX:  612-339-3061
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  970 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-250-030-1


  Query Match            100.0%;  Score 20;  DB 1;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 0.00053;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
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Db    671 TACGGCGTTTCGATGAACCC 652


RESULT  11
PCT-US95-06790-1/c
; Sequence 1, Application PC/TUS9506790
;  GENERAL INFORMATION:
;    APPLICANT:  Mayo Foundation for Medical Education and Research
;    APPLICANT:  and Hoffmann-La Roche Inc.
;    TITLE OF INVENTION:  Detection of a Genetic Locus Encoding
;    TITLE OF INVENTION:  Resistance to Rifampin
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schwegman, Lundberg & Woessner
;      STREET:  3500 IDS Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/06790
;      FILING DATE:  26-MAY-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Raasch, Kevin W.
;      REGISTRATION NUMBER:  35,651
;      REFERENCE/DOCKET NUMBER:  150.105WO1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-339-0331
;      TELEFAX:  612-339-3061
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  970 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
PCT-US95-06790-1


  Query Match            100.0%;  Score 20;  DB 5;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 0.00053;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    671 TACGGCGTTTCGATGAACCC 652


RESULT  12
US-08-750-088A-71
; Sequence 71, Application US/08750088A
; Patent No. 6329138
;  GENERAL INFORMATION:
;    APPLICANT:  DE BEENHOUWER, HANS
;    APPLICANT:  PORTAELS, FRAN OISE
;    APPLICANT:  MACHTELINCKX, LIEVE
;    APPLICANT:  JANNES, GEERT
;    APPLICANT:  ROSSAU, RUDI
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF THE ANTIBIOTIC
;    TITLE OF INVENTION:  RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  US
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/750,088A
;      FILING DATE:  21-FEB-1997
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GOLDSTEIN, JORGE A.
;      REGISTRATION NUMBER:  29,021
;      REFERENCE/DOCKET NUMBER:  1657.0010000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-750-088A-71


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  Best Local Similarity   100.0%;  Pred. No. 0.0024;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaacc 19
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Db       1 TACGGCGTTTCGATGAACC 19


RESULT  13
US-08-250-030-9
; Sequence 9, Application US/08250030
; Patent No. 5643723
;  GENERAL INFORMATION:
;    APPLICANT:  Persing, David H.
;    TITLE OF INVENTION:  Detection of a Genetic Locus Encoding
;    TITLE OF INVENTION:  Resistance to Rifampin in Mycobacterial Cultures and in
;    TITLE OF INVENTION:  Clinical Specimens
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schwegman, Lundberg & Woessner
;      STREET:  3500 IDS Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/250,030
;      FILING DATE:  26-MAY-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueting, Ann M.
;      REGISTRATION NUMBER:  33,977
;      REFERENCE/DOCKET NUMBER:  150.105US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-339-0331
;      TELEFAX:  612-339-3061
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-250-030-9


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  Best Local Similarity   100.0%;  Pred. No. 0.7;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 cgtttcgatgaaccc 20
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Db       1 CGTTTCGATGAACCC 15


RESULT  14
PCT-US95-06790-9
; Sequence 9, Application PC/TUS9506790
;  GENERAL INFORMATION:
;    APPLICANT:  Mayo Foundation for Medical Education and Research
;    APPLICANT:  and Hoffmann-La Roche Inc.
;    TITLE OF INVENTION:  Detection of a Genetic Locus Encoding
;    TITLE OF INVENTION:  Resistance to Rifampin
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schwegman, Lundberg & Woessner
;      STREET:  3500 IDS Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/06790
;      FILING DATE:  26-MAY-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Raasch, Kevin W.
;      REGISTRATION NUMBER:  35,651
;      REFERENCE/DOCKET NUMBER:  150.105WO1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-339-0331
;      TELEFAX:  612-339-3061
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
PCT-US95-06790-9


  Query Match             75.0%;  Score 15;  DB 5;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.7;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 cgtttcgatgaaccc 20
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Db       1 CGTTTCGATGAACCC 15


RESULT  15
US-08-313-185-57/c
; Sequence 57, Application US/08313185
; Patent No. 5851763
;  GENERAL INFORMATION:
;    APPLICANT:  Heym, Beate
;    APPLICANT:  Cole, Stewart
;    APPLICANT:  Young, Douglas
;    APPLICANT:  Zhang, Ying
;    APPLICANT:  Honore, Nadine
;    APPLICANT:  Telenti, Amalio
;    APPLICANT:  Bodmer, Thomas
;    TITLE OF INVENTION:  Rapid Detection of Antibiotic Resistance
```

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;    TITLE OF INVENTION:  in Mycobacterium Tuberculosis
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/313,185
;      FILING DATE:  12-OCT-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  02356.0068-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3447 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-313-185-57


  Query Match             70.0%;  Score 14;  DB 2;  Length 3447;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db    1448 GTTTCGATGAACCC 1435


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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 22:04:01 ; Search time 568.44 Seconds
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Title: US-09-786-105-3
Perfect score: 20
Sequence: 1 tacggtcggcgagctgatcc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	17	AAT12092	M. tuberculosis rp
2	20	100.0	20	21	AAA49823	Mycobacterium tube
3	20	100.0	20	21	AAA49825	Mycobacterium tube
4	20	100.0	306	19	AAX27214	RpoB gene fragment
5	20	100.0	306	19	AAX27175	RpoB gene fragment
6	20	100.0	306	19	AAX27179	RpoB gene fragment
7	20	100.0	306	19	AAX27180	RpoB gene fragment
8	20	100.0	306	24	AAS99526	Mycobacterium spec
9	20	100.0	306	24	AAS99527	Mycobacterium spec
10	20	100.0	306	24	AAS99530	Mycobacterium spec
11	20	100.0	306	24	AAS99531	Mycobacterium spec
12	20	100.0	432	14	AAQ61457	M.tuberculosis rpo
13	20	100.0	480	21	AAA49863	Mycobacterium tube
14	20	100.0	970	17	AAT09676	Mycobacterium tube
15	20	100.0	3519	22	AAH51976	Mycobacterium tube
16	20	100.0	3534	22	AAH02079	Mycobacterium tube
17	20	100.0	3853	21	AAA74651	Mycobacterium tube
18	20	100.0	3853	21	AAA89994	M. tuberculosis rp
19	19	95.0	306	19	AAX27217	RpoB gene fragment
20	19	95.0	306	24	AAS99551	Mycobacterium spec
21	19	95.0	21500	23	AAS59633	Propionibacterium
22	18.4	92.0	25	17	AAT12091	M. tuberculosis rp
23	18.4	92.0	306	19	AAX27218	RpoB gene fragment
24	18.4	92.0	306	19	AAX27193	RpoB gene fragment
25	18.4	92.0	306	19	AAX27196	RpoB gene fragment
26	18.4	92.0	306	19	AAX27177	RpoB gene fragment
27	18.4	92.0	306	19	AAX27182	RpoB gene fragment
28	18.4	92.0	306	19	AAX27183	RpoB gene fragment
29	18.4	92.0	306	24	AAS99539	Mycobacterium spec
30	18.4	92.0	306	24	AAS99557	Mycobacterium spec
31	18.4	92.0	27426	23	AAS59541	Propionibacterium
c 32	18	90.0	87	22	AAC88922	Mycobacterium tube
33	17.4	87.0	306	19	AAX27212	RpoB gene fragment
34	17.4	87.0	306	19	AAX27216	RpoB gene fragment
35	17.4	87.0	306	19	AAX27219	RpoB gene fragment
36	17.4	87.0	306	19	AAX27220	RpoB gene fragment
37	17.4	87.0	306	19	AAX27198	RpoB gene fragment
38	17.4	87.0	306	19	AAX27204	RpoB gene fragment
39	17.4	87.0	306	19	AAX27186	RpoB gene fragment
40	17.4	87.0	306	19	AAX27189	RpoB gene fragment
41	17.4	87.0	306	24	AAS99534	Mycobacterium spec
42	17.4	87.0	306	24	AAS99543	Mycobacterium spec
43	17.4	87.0	306	24	AAS99560	Mycobacterium spec
44	17.4	87.0	306	24	AAS99565	Mycobacterium spec
45	17.4	87.0	306	24	AAS99568	Mycobacterium spec

ALIGNMENTS

RESULT 1
AAT12092
ID AAT12092 standard; DNA; 20 BP.
XX
AC AAT12092;
XX
DT 10-JUL-1996 (first entry)
XX
DE M. tuberculosis rpoB gene fragment amplification primer P2.
XX
KW Antibiotic; resistance; spectrum; gene; mycobacterium;
KW determination; amplification; tuberculosis; rpoB; fragment;
KW primer; differential; hybridisation; pattern; rifampicin;
KW rifabutin; species identification; ss.
XX
OS Synthetic.
XX
PN [redacted]
XX
PD 14-DEC-1995.
XX
PF 09-JUN-1995; 95WO-EP02230.
XX
PR 09-JUN-1994; 94EP-0870093.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI De Beenhouwer H, Jannes G, Machtelinckx L, Portaels F;
PI Rossau R;
XX
DR WPI; 1996-040250/04.
XX

PT Probes and primers for determn. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene
XX
PS Claim 22; Page 39; 69pp; English.
XX
CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT12091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrids formed and
CC inferring the ARS, and opt. the spp., from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampicin and/or rifabutin resistance in M. leprae
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determn.
CC of ARS and spp. identity.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 1 tacggtcggcgagctgatcc 20

RESULT 2
AAA49823
ID AAA49823 standard; DNA; 20 BP.
XX
AC AAA49823;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene amplification primer rpoB-F.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 4; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene amplification primer rpoB-F (bp
CC 2201-2220). It is used with the reverse primer given in AAA49824
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 1 tacggtcggcgagctgatcc 20

RESULT 3
AAA49825
ID AAA49825 standard; DNA; 20 BP.
XX
AC AAA49825;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-5s.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene sequencing primer rpoB-5s (bp
CC 2201-2220). It is used with the reverse primer given in AAA49826 and
CC with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.

```
CC   These primers can be used in a method for the detection and
CC   characterization of M. tuberculosis present in a sputum sample.
CC   The method involves performing a sequencing procedure, with or
CC   without prior amplification, to detect the presence of M.
CC   tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC   and 23S genes for the presence of antibiotic-inducing mutations.
CC   If M. tuberculosis is detected, a second sequencing procedure is
CC   performed on the sample to evaluate additional genes for the
CC   presence of antibiotic resistance-inducing mutations.  Genotypic
CC   tests are rapid, sensitive and accurate providing information as to
CC   antibiotic treatment options.
XX
SQ   Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;


  Query Match           100.0%;  Score 20;  DB 21;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 1.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      1 tacggtcggcgagctgatcc 20


RESULT   4
AAX27214
ID   AAX27214 standard; DNA; 306 BP.
XX
AC   AAX27214;
XX
DT   27-MAY-1999  (first entry)
XX
DE   RpoB gene fragment.
XX
KW   RpoB gene; mycobacteria; phylogenetic tree construction;
KW   mycobacterial species identification; phylogenetic analysis; ss.
XX
OS   Mycobacteria tuberculosis.
XX
PN   WO9905316-A1.
XX
PD   04-FEB-1999.
XX
PF   28-JUL-1998;   98KR-0000228.
XX
PR   28-JUL-1997;   97KR-0035501.
XX
PA   (BION-) BIONEER CORP.
XX
PI   Kim B,  Kook Y;
XX
DR   WPI; 1998-539367/46.
XX
PT   New pair of polymerase chain reaction (PCR) primers - for
PT   sequence-specific amplification of the rpoB gene from mycobacterial
PT   species, useful for detecting and identifying mycobacterial species
XX
PS   Claim 43; Page 75-76; 91pp; English.
XX
CC   This sequence represents a mycobacterial rpoB gene fragment, that is
CC   amplified using the PCR primers of the invention. The primers form a
CC   method of detecting and identifying mycobacterial species by constructing
CC   a phylogenetic tree for the species. The use of the primers for
CC   sequence-specific amplification of the rpoB gene (encoding the beta
CC   subunit of RNA polymerase) from mycobacterial species provides an
CC   efficient way of characterising these species. In addition to
CC   phylogenetic analysis, the rpoB gene can be used as an alternative to
CC   the 16S rRNA gene because it has four subunits, which are highly
CC   conserved throughout prokaryotes. The method is particularly useful for
CC   slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
CC   susceptibility can be simultaneously determined in M. tuberculosis.
XX
SQ   Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;


  Query Match           100.0%;  Score 20;  DB 19;  Length 306;
  Best Local Similarity  100.0%;  Pred. No. 1.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 tacggtcggcgagctgatcc 24


RESULT   5
AAX27175
ID   AAX27175 standard; DNA; 306 BP.
XX
AC   AAX27175;
XX
DT   27-MAY-1999  (first entry)
XX
DE   RpoB gene fragment.
XX
KW   RpoB gene; mycobacteria; phylogenetic tree construction;
KW   mycobacterial species identification; phylogenetic analysis; ss.
XX
OS   Mycobacteria africanum.
XX
PN   WO9905316-A1.
XX
PD   04-FEB-1999.
XX
PF   28-JUL-1998;   98KR-0000228.
XX
PR   28-JUL-1997;   97KR-0035501.
XX
PA   (BION-) BIONEER CORP.
XX
PI   Kim B,  Kook Y;
XX
DR   WPI; 1998-539367/46.
XX
PT   New pair of polymerase chain reaction (PCR) primers - for
PT   sequence-specific amplification of the rpoB gene from mycobacterial
PT   species, useful for detecting and identifying mycobacterial species
XX
PS   Claim 4; Page 62-63; 91pp; English.
XX
CC   This sequence represents a mycobacterial rpoB gene fragment, that is
CC   amplified using the PCR primers of the invention. The primers form a
CC   method of detecting and identifying mycobacterial species by constructing
CC   a phylogenetic tree for the species. The use of the primers for
CC   sequence-specific amplification of the rpoB gene (encoding the beta
CC   subunit of RNA polymerase) from mycobacterial species provides an
CC   efficient way of characterising these species. In addition to
CC   phylogenetic analysis, the rpoB gene can be used as an alternative to
CC   the 16S rRNA gene because it has four subunits, which are highly
CC   conserved throughout prokaryotes. The method is particularly useful for
CC   slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
CC   susceptibility can be simultaneously determined in M. tuberculosis.
XX
SQ   Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;


  Query Match           100.0%;  Score 20;  DB 19;  Length 306;
  Best Local Similarity  100.0%;  Pred. No. 1.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 tacggtcggcgagctgatcc 24


RESULT   6
AAX27179
```

ID AAX27179 standard; DNA; 306 BP.
XX
AC AAX27179;
XX
DT 27-MAY-1999 (first entry)
XX
DE RpoB gene fragment.
XX
KW RpoB gene; mycobacteria; phylogenetic tree construction;
KW mycobacterial species identification; phylogenetic analysis; ss.
XX
OS Mycobacteria bovis.
XX
PN WO9905316-A1.
XX
PD 04-FEB-1999.
XX
PF 28-JUL-1998; 98KR-0000228.
XX
PR 28-JUL-1997; 97KR-0035501.
XX
PA (BION-) BIONEER CORP.
XX
PI Kim B, Kook Y;
XX
DR WPI; 1998-539367/46.
XX
PT New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the rpoB gene from mycobacterial
PT species, useful for detecting and identifying mycobacterial species
XX
PS Claim 8; Page 64; 91pp; English.
XX
CC This sequence represents a mycobacterial rpoB gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the rpoB gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterising these species. In addition to
CC phylogenetic analysis, the rpoB gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in M. tuberculosis.
XX
SQ Sequence 306 BP; 56 A; 96 C; 107 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 7
AAX27180
ID AAX27180 standard; DNA; 306 BP.
XX
AC AAX27180;
XX
DT 27-MAY-1999 (first entry)
XX
DE RpoB gene fragment.
XX
KW RpoB gene; mycobacteria; phylogenetic tree construction;
KW mycobacterial species identification; phylogenetic analysis; ss.
XX
OS Mycobacteria bovis.
XX
PN WO9905316-A1.
XX
PD 04-FEB-1999.
XX
PF 28-JUL-1998; 98KR-0000228.
XX
PR 28-JUL-1997; 97KR-0035501.
XX
PA (BION-) BIONEER CORP.
XX
PI Kim B, Kook Y;
XX
DR WPI; 1998-539367/46.
XX
PT New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the rpoB gene from mycobacterial
PT species, useful for detecting and identifying mycobacterial species
XX
PS Claim 9; Page 64; 91pp; English.
XX
CC This sequence represents a mycobacterial rpoB gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the rpoB gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterising these species. In addition to
CC phylogenetic analysis, the rpoB gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in M. tuberculosis.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 8
AAS99526
ID AAS99526 standard; DNA; 306 BP.
XX
AC AAS99526;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #1.
XX
KW Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200192573-A1.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-KR00904.
XX
PR 30-MAY-2000; 2000KR-0029369.
XX
PA (BIOM-) BIOMEDLAB CO LTD.
XX
PI Kim H, Kim N, Yoon S, Kim J, Park M;
XX

DR WPI; 2002-075472/10.
XX
PT Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -
XX
PS Disclosure; Page 21; 74pp; English.
XX
CC The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 9
AAS99527
ID AAS99527 standard; DNA; 306 BP.
XX
AC AAS99527;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #2.
XX
KW Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
OS Mycobacterium africanum.
XX
PN WO200192573-A1.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-KR00904.
XX
PR 30-MAY-2000; 2000KR-0029369.
XX
PA (BIOM-) BIOMEDLAB CO LTD.
XX
PI Kim H, Kim N, Yoon S, Kim J, Park M;
XX
DR WPI; 2002-075472/10.
XX
PT Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -
XX
PS Disclosure; Page 21; 74pp; English.
XX
CC The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 10
AAS99530
ID AAS99530 standard; DNA; 306 BP.
XX
AC AAS99530;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #5.
XX
KW Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
OS Mycobacterium bovis.
XX
PN WO200192573-A1.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-KR00904.
XX
PR 30-MAY-2000; 2000KR-0029369.
XX
PA (BIOM-) BIOMEDLAB CO LTD.
XX
PI Kim H, Kim N, Yoon S, Kim J, Park M;
XX
DR WPI; 2002-075472/10.
XX
PT Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -
XX
PS Disclosure; Page 21; 74pp; English.
XX
CC The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of

CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 11
AAS99531
ID AAS99531 standard; DNA; 306 BP.
XX
AC AAS99531;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #6.
XX
KW Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
OS Mycobacterium bovis.
XX
PN WO200192573-A1.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-KR00904.
XX
PR 30-MAY-2000; 2000KR-0029369.
XX
PA (BIOM-) BIOMEDLAB CO LTD.
XX
PI Kim H, Kim N, Yoon S, Kim J, Park M;
XX
DR WPI; 2002-075472/10.
XX
PT Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -
XX
PS Disclosure; Page 21; 74pp; English.
XX
CC The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 12
AAQ61457
ID AAQ61457 standard; DNA; 432 BP.
XX
AC AAQ61457;
XX
DT 17-MAY-1994 (first entry)
XX
DE M.tuberculosis rpoB gene fragment.
XX
KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KW mutant; ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9322454-A.
XX
PD 11-NOV-1993.
XX
PF 30-APR-1993; 93WO-EP01063.
XX
PR 17-SEP-1992; 92FR-0011098.
PR 30-APR-1992; 92US-0875940.
PR 14-AUG-1992; 92US-0929206.
PR 16-APR-1993; 93FR-0004545.
XX
PA (ASSI-) ASSISTANCE PUBLIQUE.
PA (INSP) INST PASTEUR.
PA (MEDI-) MEDICAL RES COUNCIL.
PA (UYBE-) UNIV BERNE.
PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
PI Young D, Zhang Y;
XX
DR WPI; 1993-368812/46.
DR P-PSDB; AAR51372.
XX
PT Rapid detection of antibiotic resistance in Mycobacteria - esp.
PT isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in katG, rpoB or rpsL genes
XX
PS Example 2; Fig 13; 97pp; English.
XX
CC PCR amplification was used to obtain rpoB genes from rifampicin-
CC resistant Mycobacterium leprae strains. A comparison with the
CC sequence of the rpoB gene from sensitive strains (AAQ51532) revealed
CC mutations in the region encoding amino acids 400-450. The corresp.
CC region was isolated from M.tuberculosis (AAQ61457). A common
CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
SQ Sequence 432 BP; 78 A; 139 C; 148 G; 67 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20

```
                    ||||||||||||||||||||
Db      18 tacggtcggcgagctgatcc 37


RESULT  13
AAA49863
ID   AAA49863 standard; DNA; 480 BP.
XX
AC   AAA49863;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Mycobacterium tuberculosis rpoB gene (rifampin resistance).
XX
KW   Antibiotic resistance; rpoB gene; rifampin resistance; ss.
XX
OS   Mycobacterium tuberculosis.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     complement(41..60)
FT                   /*tag=  a
FT                   /note= "primer of AAA49823"
FT   primer_bind     372..391
FT                   /*tag=  b
FT                   /note= "primer of AAA49824"
XX
PN   WO200036142-A1.
XX
PD   22-JUN-2000.
XX
PF   10-DEC-1999;   99WO-CA01177.
XX
PR   11-DEC-1998;   98US-0111794.
XX
PA   (VISI-) VISIBLE GENETICS INC.
XX
PI   Shipman R;
XX
DR   WPI; 2000-431611/37.
XX
PT   Method for the detection and characterization of Mycobacterium
PT   tuberculosis with antibiotic resistance in a sample -
XX
PS   Disclosure; Page 5; 43pp; English.
XX
CC   The present sequence is that of the Mycobacterium tuberculosis
CC   rpoB (rifampin resistance) gene (bp2161-2640).  Amplification and
CC   cycle sequencing primers (see AAA49823-62) are used for the detection
CC   and analysis of antibiotic resistance-associated mutations in
CC   defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC   (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC   (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC   (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC   These primers can be used in a method for the detection and
CC   characterization of M. tuberculosis present in a sputum sample.
CC   The method involves performing a sequencing procedure, with or
CC   without prior amplification, to detect the presence of M.
CC   tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC   and 23S genes for the presence of antibiotic-inducing mutations.
CC   If M. tuberculosis is detected, a second sequencing procedure is
CC   performed on the sample to evaluate additional genes for the
CC   presence of antibiotic resistance-inducing mutations.  Genotypic
CC   tests are rapid, sensitive and accurate providing information as to
CC   antibiotic treatment options.
XX
SQ   Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 21;  Length 480;
  Best Local Similarity   100.0%;  Pred. No. 1.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggtcggcgagctgatcc 20
```

```
                    ||||||||||||||||||||
Db      41 tacggtcggcgagctgatcc 60


RESULT  14
AAT09676
ID   AAT09676 standard; DNA; 970 BP.
XX
AC   AAT09676;
XX
DT   15-OCT-1996  (first entry)
XX
DE   Mycobacterium tuberculosis rpoB gene DNA sequence.
XX
KW   Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;
KW   polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.
XX
OS   Mycobacterium tuberculosis.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     10..27
FT                   /*tag=  a
FT                   /note= "primer FENLFF"
FT   primer_bind     226..243
FT                   /*tag=  b
FT                   /note= "primer DDIDHL"
FT   primer_bind     226..240
FT                   /*tag=  c
FT                   /note= "primer DDIDH"
FT   primer_bind     338..364
FT                   /*tag=  d
FT                   /note= "primer rpo95"
FT   primer_bind     348..373
FT                   /*tag=  e
FT                   /note= "primer rpo105"
FT   primer_bind     354..373
FT                   /*tag=  f
FT                   /note= "primer KY290"
FT   misc_feature    372..373
FT                   /*tag=  g
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    433..434
FT                   /*tag=  h
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    438
FT                   /*tag=  i
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    468..469
FT                   /*tag=  j
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    486
FT                   /*tag=  k
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    501
FT                   /*tag=  l
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    516
FT                   /*tag=  m
FT                   /note= "M. tuberculosis signature nucleotide"
FT   primer_bind     516..535
FT                   /*tag=  n
FT                   /note= "primer rpo273"
FT   misc_feature    525
FT                   /*tag=  o
FT                   /note= "M. tuberculosis signature nucleotide"
FT   primer_bind     525..541
FT                   /*tag=  p
FT                   /note= "primer KY292"
FT   primer_bind     536..562
FT                   /*tag=  q
FT                   /note= "primer rpo293"
FT   primer_bind     640..666
FT                   /*tag=  r
```

```
FT                   /note= "primer rpo397"
FT   primer_bind     952..966
FT                   /*tag= s
FT                   /note= "primer NMQRQ-1"
FT   primer_bind     952..966
FT                   /*tag= t
FT                   /note= "primer NMQRQ-2"
XX
PN   WO9533074-A1.
XX
PD   07-DEC-1995.
XX
PF   26-MAY-1995;   95WO-US06790.
XX
PR   26-MAY-1994;   94US-0250030.
XX
PA   (HOFF ) HOFFMANN LA ROCHE INC.
PA   (MAYO-) MAYO FOUNDATION.
XX
PI   Felmlee TA,  Hunt JM,  Persing DH,  Roberts GD,  Whelen AC;
PI   Young KKY;
XX
DR   WPI; 1996-030581/03.
XX
PT   Detection of Mycobacterium tuberculosis - by amplifying sample DNA
PT   with a primer set that targets portions of the gene encoding rpoB.
XX
PS   Disclosure; Fig.3; 54pp; English.
XX
CC   This oligonucleotide DNA primer is specific for Mycobacterium
CC   tuberculosis, and may be used to amplify a sample DNA by targeting
CC   a portion of the gene encoding rpoB.  The 1st several bases comprise a
CC   nonhybridizing tail consisting of filler bases followed by
CC   a restriction site incorporated to facilitate cloning using the
CC   amplicon at a later date, if desired.  The remaining bases hybridize
CC   to bacterial rpoB DNA.  The method provides for the detection of M.
CC   tuberculosis and the concurrent determination of its drug
CC   susceptibility, particularly to rifamycin.  The method can provide
CC   often greater than 95% sensitivity and 100% specificity.  The
CC   biological sample is a fluid or tissue sample from a human.
XX
SQ   Sequence 970 BP; 182 A; 302 C; 330 G; 156 T; 0 other;


  Query Match            100.0%;  Score 20;  DB 17;  Length 970;
  Best Local Similarity  100.0%;  Pred. No. 1.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db    261 tacggtcggcgagctgatcc 280


RESULT  15
AAH51976
ID   AAH51976 standard; DNA; 3519 BP.
XX
AC   AAH51976;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Mycobacterium tuberculosis potential drug target gene SEQ ID 30.
XX
KW   Drug target; growth; organism viability; characterisation; ds.
XX
OS   Mycobacterium tuberculosis.
XX
PN   WO200135317-A1.
XX
PD   17-MAY-2001.
XX
PF   13-NOV-2000; 2000WO-US31152.
XX
PR   12-NOV-1999;   99US-0165086.
PR   12-NOV-1999;   99US-0165124.
PR   01-FEB-2000; 2000US-0179531.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Eisenberg D,  Rotstein SH,  Marcotte EM;
XX
DR   WPI; 2001-329193/34.
DR   P-PSDB; AAG81125.
XX
PT   Identifying nucleotide or polypeptide sequence for use as drug target,
PT   involves providing algorithm that analyzes a functional relationship
PT   between nucleotide or polypeptide sequences, and comparing the
PT   sequences -
XX
PS   Disclosure; Page 68-69; 207pp; English.
XX
CC   This invention relates to a method for identifying a nucleotide or
CC   polypeptide sequence that may be a drug target, or essential for growth
CC   or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
CC   represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
CC   tuberculosis proteins which are potential drug targets. The DNA and
CC   protein sequences are used to illustrate the method of the invention. The
CC   method involves providing an unknown nucleotide or polypeptide sequences,
CC   and comparing it to a number of sequences along with at least one
CC   algorithm capable of analysing a functional relationship between
CC   nucleotide and polypeptide sequences. The method is useful for
CC   characterising the function of nucleic acids and polypeptides that may be
CC   useful as a target for a drug or essential for the growth or viability of
CC   an organism.
XX
SQ   Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;


  Query Match            100.0%;  Score 20;  DB 22;  Length 3519;
  Best Local Similarity  100.0%;  Pred. No. 1.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db   1119 tacggtcggcgagctgatcc 1138


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Job time: 8061 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 19:49:40 ; Search time 568.44 Seconds
(without alignments)
60.408 Million cell updates/sec

Title: US-09-786-105-1
Perfect score: 20
Sequence: 1 tacggtcggcgagctgatcc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	17	AAT12092	M. tuberculosis rp
2	20	100.0	20	21	AAA49823	Mycobacterium tube
3	20	100.0	20	21	AAA49825	Mycobacterium tube
4	20	100.0	306	19	AAX27214	RpoB gene fragment
5	20	100.0	306	19	AAX27175	RpoB gene fragment
6	20	100.0	306	19	AAX27179	RpoB gene fragment
7	20	100.0	306	19	AAX27180	RpoB gene fragment
8	20	100.0	306	24	AAS99526	Mycobacterium spec
9	20	100.0	306	24	AAS99527	Mycobacterium spec
10	20	100.0	306	24	AAS99530	Mycobacterium spec
11	20	100.0	306	24	AAS99531	Mycobacterium spec
12	20	100.0	432	14	AAQ61457	M.tuberculosis rpo
13	20	100.0	480	21	AAA49863	Mycobacterium tube
14	20	100.0	970	17	AAT09676	Mycobacterium tube
15	20	100.0	3519	22	AAH51976	Mycobacterium tube
16	20	100.0	3534	22	AAH02079	Mycobacterium tube
17	20	100.0	3853	21	AAA74651	Mycobacterium tube
18	20	100.0	3853	21	AAA89994	M. tuberculosis rp
19	19	95.0	306	19	AAX27217	RpoB gene fragment
20	19	95.0	306	24	AAS99551	Mycobacterium spec
21	19	95.0	21500	23	AAS59633	Propionibacterium
22	18.4	92.0	25	17	AAT12091	M. tuberculosis rp
23	18.4	92.0	306	19	AAX27218	RpoB gene fragment
24	18.4	92.0	306	19	AAX27193	RpoB gene fragment
25	18.4	92.0	306	19	AAX27196	RpoB gene fragment
26	18.4	92.0	306	19	AAX27177	RpoB gene fragment
27	18.4	92.0	306	19	AAX27182	RpoB gene fragment
28	18.4	92.0	306	19	AAX27183	RpoB gene fragment
29	18.4	92.0	306	24	AAS99539	Mycobacterium spec
30	18.4	92.0	306	24	AAS99557	Mycobacterium spec
31	18.4	92.0	27426	23	AAS59541	Propionibacterium
c 32	18	90.0	87	22	AAC88922	Mycobacterium tube
33	17.4	87.0	306	19	AAX27212	RpoB gene fragment
34	17.4	87.0	306	19	AAX27216	RpoB gene fragment
35	17.4	87.0	306	19	AAX27219	RpoB gene fragment
36	17.4	87.0	306	19	AAX27220	RpoB gene fragment
37	17.4	87.0	306	19	AAX27198	RpoB gene fragment
38	17.4	87.0	306	19	AAX27204	RpoB gene fragment
39	17.4	87.0	306	19	AAX27186	RpoB gene fragment
40	17.4	87.0	306	19	AAX27189	RpoB gene fragment
41	17.4	87.0	306	24	AAS99534	Mycobacterium spec
42	17.4	87.0	306	24	AAS99543	Mycobacterium spec
43	17.4	87.0	306	24	AAS99560	Mycobacterium spec
44	17.4	87.0	306	24	AAS99565	Mycobacterium spec
45	17.4	87.0	306	24	AAS99568	Mycobacterium spec

ALIGNMENTS

RESULT 1
AAT12092
ID AAT12092 standard; DNA; 20 BP.
XX
AC AAT12092;
XX
DT 10-JUL-1996 (first entry)
XX
DE M. tuberculosis rpoB gene fragment amplification primer P2.
XX
KW Antibiotic; resistance; spectrum; gene; mycobacterium;
KW determination; amplification; tuberculosis; rpoB; fragment;
KW primer; differential; hybridisation; pattern; rifampicin;
KW rifabutin; species identification; ss.
XX
OS Synthetic.
XX
PN [redacted]WO9538851-A2.
XX
PD 14-DEC-1995.
XX
PF [redacted]09-JUN-1995; 95WO-EP02230.
XX
PR 09-JUN-1994; 94EP-0870093.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI De Beenhouwer H, Jannes G, Machtelinckx L, Portaels F;
PI Rossau R;
XX
DR WPI; 1996-040250/04.
XX

PT Probes and primers for determn. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene
XX
PS Claim 22; Page 39; 69pp; English.
XX
CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT12091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrids formed and
CC inferring the ARS, and opt. the spp., from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampicin and/or rifabutin resistance in M. leprae
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determn.
CC of ARS and spp. identity.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 1 tacggtcggcgagctgatcc 20

RESULT 2
AAA49823
ID AAA49823 standard; DNA; 20 BP.
XX
AC AAA49823;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene amplification primer rpoB-F.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 4; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene amplification primer rpoB-F (bp
CC 2201-2220). It is used with the reverse primer given in AAA49824
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 1 tacggtcggcgagctgatcc 20

RESULT 3
AAA49825
ID AAA49825 standard; DNA; 20 BP.
XX
AC AAA49825;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-5s.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene sequencing primer rpoB-5s (bp
CC 2201-2220). It is used with the reverse primer given in AAA49826 and
CC with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.

CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 1 tacggtcggcgagctgatcc 20

RESULT 4
AAX27214
ID AAX27214 standard; DNA; 306 BP.
XX
AC AAX27214;
XX
DT 27-MAY-1999 (first entry)
XX
DE RpoB gene fragment.
XX
KW RpoB gene; mycobacteria; phylogenetic tree construction;
KW mycobacterial species identification; phylogenetic analysis; ss.
XX
OS Mycobacteria tuberculosis.
XX
PN WO9905316-A1.
XX
PD 04-FEB-1999.
XX
PF 28-JUL-1998; 98KR-0000228.
XX
PR 28-JUL-1997; 97KR-0035501.
XX
PA (BION-) BIONEER CORP.
XX
PI Kim B, Kook Y;
XX
DR WPI; 1998-539367/46.
XX
PT New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the rpoB gene from mycobacterial
PT species, useful for detecting and identifying mycobacterial species
XX
PS Claim 43; Page 75-76; 91pp; English.
XX
CC This sequence represents a mycobacterial rpoB gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the rpoB gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterising these species. In addition to
CC phylogenetic analysis, the rpoB gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in M. tuberculosis.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 5
AAX27175
ID AAX27175 standard; DNA; 306 BP.
XX
AC AAX27175;
XX
DT 27-MAY-1999 (first entry)
XX
DE RpoB gene fragment.
XX
KW RpoB gene; mycobacteria; phylogenetic tree construction;
KW mycobacterial species identification; phylogenetic analysis; ss.
XX
OS Mycobacteria africanum.
XX
PN WO9905316-A1.
XX
PD 04-FEB-1999.
XX
PF 28-JUL-1998; 98KR-0000228.
XX
PR 28-JUL-1997; 97KR-0035501.
XX
PA (BION-) BIONEER CORP.
XX
PI Kim B, Kook Y;
XX
DR WPI; 1998-539367/46.
XX
PT New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the rpoB gene from mycobacterial
PT species, useful for detecting and identifying mycobacterial species
XX
PS Claim 4; Page 62-63; 91pp; English.
XX
CC This sequence represents a mycobacterial rpoB gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the rpoB gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterising these species. In addition to
CC phylogenetic analysis, the rpoB gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in M. tuberculosis.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 6
AAX27179

ID AAX27179 standard; DNA; 306 BP.
XX
AC AAX27179;
XX
DT 27-MAY-1999 (first entry)
XX
DE RpoB gene fragment.
XX
KW RpoB gene; mycobacteria; phylogenetic tree construction;
KW mycobacterial species identification; phylogenetic analysis; ss.
XX
OS Mycobacteria bovis.
XX
PN WO9905316-A1.
XX
PD 04-FEB-1999.
XX
PF 28-JUL-1998; 98KR-0000228.
XX
PR 28-JUL-1997; 97KR-0035501.
XX
PA (BION-) BIONEER CORP.
XX
PI Kim B, Kook Y;
XX
DR WPI; 1998-539367/46.
XX
PT New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the rpoB gene from mycobacterial
PT species, useful for detecting and identifying mycobacterial species
XX
PS Claim 8; Page 64; 91pp; English.
XX
CC This sequence represents a mycobacterial rpoB gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the rpoB gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterising these species. In addition to
CC phylogenetic analysis, the rpoB gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in M. tuberculosis.
XX
SQ Sequence 306 BP; 56 A; 96 C; 107 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 7
AAX27180
ID AAX27180 standard; DNA; 306 BP.
XX
AC AAX27180;
XX
DT 27-MAY-1999 (first entry)
XX
DE RpoB gene fragment.
XX
KW RpoB gene; mycobacteria; phylogenetic tree construction;
KW mycobacterial species identification; phylogenetic analysis; ss.
XX
OS Mycobacteria bovis.
XX
PN WO9905316-A1.
XX
PD 04-FEB-1999.
XX
PF 28-JUL-1998; 98KR-0000228.
XX
PR 28-JUL-1997; 97KR-0035501.
XX
PA (BION-) BIONEER CORP.
XX
PI Kim B, Kook Y;
XX
DR WPI; 1998-539367/46.
XX
PT New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the rpoB gene from mycobacterial
PT species, useful for detecting and identifying mycobacterial species
XX
PS Claim 9; Page 64; 91pp; English.
XX
CC This sequence represents a mycobacterial rpoB gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the rpoB gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterising these species. In addition to
CC phylogenetic analysis, the rpoB gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in M. tuberculosis.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 8
AAS99526
ID AAS99526 standard; DNA; 306 BP.
XX
AC AAS99526;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #1.
XX
KW Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200192573-A1.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-KR00904.
XX
PR 30-MAY-2000; 2000KR-0029369.
XX
PA (BIOM-) BIOMEDLAB CO LTD.
XX
PI Kim H, Kim N, Yoon S, Kim J, Park M;
XX

DR WPI; 2002-075472/10.
XX
PT Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -
XX
PS Disclosure; Page 21; 74pp; English.
XX
CC The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 9
AAS99527
ID AAS99527 standard; DNA; 306 BP.
XX
AC AAS99527;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #2.
XX
KW Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
OS Mycobacterium africanum.
XX
PN WO200192573-A1.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-KR00904.
XX
PR 30-MAY-2000; 2000KR-0029369.
XX
PA (BIOM-) BIOMEDLAB CO LTD.
XX
PI Kim H, Kim N, Yoon S, Kim J, Park M;
XX
DR WPI; 2002-075472/10.
XX
PT Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -
XX
PS Disclosure; Page 21; 74pp; English.
XX
CC The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 10
AAS99530
ID AAS99530 standard; DNA; 306 BP.
XX
AC AAS99530;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #5.
XX
KW Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
OS Mycobacterium bovis.
XX
PN WO200192573-A1.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-KR00904.
XX
PR 30-MAY-2000; 2000KR-0029369.
XX
PA (BIOM-) BIOMEDLAB CO LTD.
XX
PI Kim H, Kim N, Yoon S, Kim J, Park M;
XX
DR WPI; 2002-075472/10.
XX
PT Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -
XX
PS Disclosure; Page 21; 74pp; English.
XX
CC The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of

CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 11
AAS99531
ID AAS99531 standard; DNA; 306 BP.
XX
AC AAS99531;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #6.
XX
KW Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
OS Mycobacterium bovis.
XX
PN WO200192573-A1.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-KR00904.
XX
PR 30-MAY-2000; 2000KR-0029369.
XX
PA (BIOM-) BIOMEDLAB CO LTD.
XX
PI Kim H, Kim N, Yoon S, Kim J, Park M;
XX
DR WPI; 2002-075472/10.
XX
PT Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -
XX
PS Disclosure; Page 21; 74pp; English.
XX
CC The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 12
AAQ61457
ID AAQ61457 standard; DNA; 432 BP.
XX
AC AAQ61457;
XX
DT 17-MAY-1994 (first entry)
XX
DE M.tuberculosis rpoB gene fragment.
XX
KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KW mutant; ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9322454-A.
XX
PD 11-NOV-1993.
XX
PF 30-APR-1993; 93WO-EP01063.
XX
PR 17-SEP-1992; 92FR-0011098.
PR 30-APR-1992; 92US-0875940.
PR 14-AUG-1992; 92US-0929206.
PR 16-APR-1993; 93FR-0004545.
XX
PA (ASSI-) ASSISTANCE PUBLIQUE.
PA (INSP) INST PASTEUR.
PA (MEDI-) MEDICAL RES COUNCIL.
PA (UYBE-) UNIV BERNE.
PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
PI Young D, Zhang Y;
XX
DR WPI; 1993-368812/46.
DR P-PSDB; AAR51372.
XX
PT Rapid detection of antibiotic resistance in Mycobacteria - esp.
PT isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in katG, rpoB or rpsL genes
XX
PS Example 2; Fig 13; 97pp; English.
XX
CC PCR amplification was used to obtain rpoB genes from rifampicin-
CC resistant Mycobacterium leprae strains. A comparison with the
CC sequence of the rpoB gene from sensitive strains (AAQ51532) revealed
CC mutations in the region encoding amino acids 400-450. The corresp.
CC region was isolated from M.tuberculosis (AAQ61457). A common
CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
SQ Sequence 432 BP; 78 A; 139 C; 148 G; 67 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20

```
                    ||||||||||||||||||||
Db      18 tacggtcggcgagctgatcc 37


RESULT  13
AAA49863
ID   AAA49863 standard; DNA; 480 BP.
XX
AC   AAA49863;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Mycobacterium tuberculosis rpoB gene (rifampin resistance).
XX
KW   Antibiotic resistance; rpoB gene; rifampin resistance; ss.
XX
OS   Mycobacterium tuberculosis.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     complement(41..60)
FT                   /*tag=  a
FT                   /note= "primer of AAA49823"
FT   primer_bind     372..391
FT                   /*tag=  b
FT                   /note= "primer of AAA49824"
XX
PN   WO200036142-A1.
XX
PD   22-JUN-2000.
XX
PF   10-DEC-1999;   99WO-CA01177.
XX
PR   11-DEC-1998;   98US-0111794.
XX
PA   (VISI-) VISIBLE GENETICS INC.
XX
PI   Shipman R;
XX
DR   WPI; 2000-431611/37.
XX
PT   Method for the detection and characterization of Mycobacterium
PT   tuberculosis with antibiotic resistance in a sample -
XX
PS   Disclosure; Page 5; 43pp; English.
XX
CC   The present sequence is that of the Mycobacterium tuberculosis
CC   rpoB (rifampin resistance) gene (bp2161-2640).  Amplification and
CC   cycle sequencing primers (see AAA49823-62) are used for the detection
CC   and analysis of antibiotic resistance-associated mutations in
CC   defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC   (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC   (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC   (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC   These primers can be used in a method for the detection and
CC   characterization of M. tuberculosis present in a sputum sample.
CC   The method involves performing a sequencing procedure, with or
CC   without prior amplification, to detect the presence of M.
CC   tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC   and 23S genes for the presence of antibiotic-inducing mutations.
CC   If M. tuberculosis is detected, a second sequencing procedure is
CC   performed on the sample to evaluate additional genes for the
CC   presence of antibiotic resistance-inducing mutations.  Genotypic
CC   tests are rapid, sensitive and accurate providing information as to
CC   antibiotic treatment options.
XX
SQ   Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 21;  Length 480;
  Best Local Similarity   100.0%;  Pred. No. 1.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggtcggcgagctgatcc 20
```

```
                    ||||||||||||||||||||
Db      41 tacggtcggcgagctgatcc 60


RESULT  14
AAT09676
ID   AAT09676 standard; DNA; 970 BP.
XX
AC   AAT09676;
XX
DT   15-OCT-1996  (first entry)
XX
DE   Mycobacterium tuberculosis rpoB gene DNA sequence.
XX
KW   Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;
KW   polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.
XX
OS   Mycobacterium tuberculosis.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     10..27
FT                   /*tag=  a
FT                   /note= "primer FENLFF"
FT   primer_bind     226..243
FT                   /*tag=  b
FT                   /note= "primer DDIDHL"
FT   primer_bind     226..240
FT                   /*tag=  c
FT                   /note= "primer DDIDH"
FT   primer_bind     338..364
FT                   /*tag=  d
FT                   /note= "primer rpo95"
FT   primer_bind     348..373
FT                   /*tag=  e
FT                   /note= "primer rpo105"
FT   primer_bind     354..373
FT                   /*tag=  f
FT                   /note= "primer KY290"
FT   misc_feature    372..373
FT                   /*tag=  g
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    433..434
FT                   /*tag=  h
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    438
FT                   /*tag=  i
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    468..469
FT                   /*tag=  j
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    486
FT                   /*tag=  k
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    501
FT                   /*tag=  l
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    516
FT                   /*tag=  m
FT                   /note= "M. tuberculosis signature nucleotide"
FT   primer_bind     516..535
FT                   /*tag=  n
FT                   /note= "primer rpo273"
FT   misc_feature    525
FT                   /*tag=  o
FT                   /note= "M. tuberculosis signature nucleotide"
FT   primer_bind     525..541
FT                   /*tag=  p
FT                   /note= "primer KY292"
FT   primer_bind     536..562
FT                   /*tag=  q
FT                   /note= "primer rpo293"
FT   primer_bind     640..666
FT                   /*tag=  r
```

FT /note= "primer rpo397"
FT primer_bind 952..966
FT /*tag= s
FT /note= "primer NMQRQ-1"
FT primer_bind 952..966
FT /*tag= t
FT /note= "primer NMQRQ-2"
XX
PN WO9533074-A1.
XX
PD 07-DEC-1995.
XX
PF 26-MAY-1995; 95WO-US06790.
XX
PR 26-MAY-1994; 94US-0250030.
XX
PA (HOFF) HOFFMANN LA ROCHE INC.
PA (MAYO-) MAYO FOUNDATION.
XX
PI Felmlee TA, Hunt JM, Persing DH, Roberts GD, Whelen AC;
PI Young KKY;
XX
DR WPI; 1996-030581/03.
XX
PT Detection of Mycobacterium tuberculosis - by amplifying sample DNA
PT with a primer set that targets portions of the gene encoding rpoB.
XX
PS Disclosure; Fig.3; 54pp; English.
XX
CC This oligonucleotide DNA primer is specific for Mycobacterium
CC tuberculosis, and may be used to amplify a sample DNA by targeting
CC a portion of the gene encoding rpoB. The 1st several bases comprise a
CC nonhybridizing tail consisting of filler bases followed by
CC a restriction site incorporated to facilitate cloning using the
CC amplicon at a later date, if desired. The remaining bases hybridize
CC to bacterial rpoB DNA. The method provides for the detection of M.
CC tuberculosis and the concurrent determination of its drug
CC susceptibility, particularly to rifamycin. The method can provide
CC often greater than 95% sensitivity and 100% specificity. The
CC biological sample is a fluid or tissue sample from a human.
XX
SQ Sequence 970 BP; 182 A; 302 C; 330 G; 156 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 970;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 261 tacggtcggcgagctgatcc 280

RESULT 15
AAH51976
ID AAH51976 standard; DNA; 3519 BP.
XX
AC AAH51976;
XX
DT 04-SEP-2001 (first entry)
XX
DE Mycobacterium tuberculosis potential drug target gene SEQ ID 30.
XX
KW Drug target; growth; organism viability; characterisation; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200135317-A1.
XX
PD 17-MAY-2001.
XX
PF 13-NOV-2000; 2000WO-US31152.
XX
PR 12-NOV-1999; 99US-0165086.
PR 12-NOV-1999; 99US-0165124.
PR 01-FEB-2000; 2000US-0179531.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Eisenberg D, Rotstein SH, Marcotte EM;
XX
DR WPI; 2001-329193/34.
DR P-PSDB; AAG81125.
XX
PT Identifying nucleotide or polypeptide sequence for use as drug target,
PT involves providing algorithm that analyzes a functional relationship
PT between nucleotide or polypeptide sequences, and comparing the
PT sequences -
XX
PS Disclosure; Page 68-69; 207pp; English.
XX
CC This invention relates to a method for identifying a nucleotide or
CC polypeptide sequence that may be a drug target, or essential for growth
CC or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
CC represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
CC tuberculosis proteins which are potential drug targets. The DNA and
CC protein sequences are used to illustrate the method of the invention. The
CC method involves providing an unknown nucleotide or polypeptide sequences,
CC and comparing it to a number of sequences along with at least one
CC algorithm capable of analysing a functional relationship between
CC nucleotide and polypeptide sequences. The method is useful for
CC characterising the function of nucleic acids and polypeptides that may be
CC useful as a target for a drug or essential for the growth or viability of
CC an organism.
XX
SQ Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 3519;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 1119 tacggtcggcgagctgatcc 1138

Search completed: August 7, 2002, 22:03:58
Job time: 8058 sec

178

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BASE COUNT 969 a 1534 c 1691 g 890 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 5084;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
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Db 2611 TACGGCGTTTCGATGAACCC 2592

RESULT 15
AE006964/c
LOCUS AE006964 19352 bp DNA linear BCT 27-APR-2001
DEFINITION Mycobacterium tuberculosis CDC1551, section 50 of 280 of the complete genome.
ACCESSION AE006964 AE000516
VERSION AE006964.1 GI:13880217
KEYWORDS .
SOURCE Mycobacterium tuberculosis CDC1551.
ORGANISM Mycobacterium tuberculosis CDC1551
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 19352)
AUTHORS Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O., Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E., Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M., Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H., Gill,J., Mikula,A. and Bishai,W.
TITLE Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 19352)
AUTHORS Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O., Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E., Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M., Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H., Gill,J., Mikula,A. and Bishai,W.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
FEATURES Location/Qualifiers
source 1. .19352
/organism="Mycobacterium tuberculosis CDC1551"
/strain="CDC1551"
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/note="clinical strain"
gene 163. .3699
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CDS 163. .3699
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/db_xref="GI:13880218"
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IYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARVGRYKVNKKLGLHVGEPITSSTLT
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gene 3744. .7694
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CDS 3744. .7694
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/note="similar to SP:P37871; identified by sequence similarity; putative"
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LFKPFVMKRLVDLNHAQNIKSAKRMVERQRPQVWDVLEEVIAEHPVLLNRAPTLHRLG
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GVLSVRAKIKVRLTQLRPPVEIEAELFGHSGWQPGDAWMAETTLGRVMFNELLPLGYP
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RKKEILDHYEERADKVEKQFQRGALNHDERNEALVEIWKEATDEVGQALREHYPDDNP
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RKGLADTALRTADSGYLTRRLVDVSQDVIVREHDCQTERGIVVELAERAPDGTLIRDP
YIETSAYARTLGTDAVDEAGNVIVERGQDLGDPEIDALLAAGITQVKVRSVLTCATST
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gene complement(7691. .8065)
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CDS complement(7691. .8065)
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gene complement(8058. .9972)
/gene="MT0698"
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  Best Local Similarity   100.0%;  Pred. No. 0.057;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
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Db    1547 TACGGCGTTTCGATGAACCC 1528


RESULT 13
MTU12205/c
LOCUS       MTU12205                3853 bp    DNA     linear   BCT 02-MAR-2000
DEFINITION  Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
            gene, partial cds.
ACCESSION   U12205
VERSION     U12205.1  GI:515684
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 3853)
  AUTHORS   Imboden,P., Troller,R., Marchesi,F., Telenti,A., Bodmer,T.,
            Cole,S., Schopfer,K. and Burkart,T.
  TITLE     The rpoB gene of Mycobacterium tuberculosis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3853)
  AUTHORS   Imboden,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-1994) Paul Imboden, Institute for Medical
            Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
            3010, Switzerland
FEATURES             Location/Qualifiers
     source          1. .3853
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                     /strain="H37Rv"
                     /db_xref="taxon:1773"
     gene            576. .>3853
                     /gene="rpoB"
     CDS             576. .>3853
                     /gene="rpoB"
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                     RDTVGVRIDRKRRQPVTVLLKALGWTSEQIVERFGFSEIMRSTLEKDNTVGTDEALLD
                     IYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARVGRYKVNKKLGLHVGEPITSSTLT
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                     LVGTGMELRAAIDAATSSSQESGVIEEVSADYITVMHDNGTRRTYRMRKFARSNHGTC
                     ANQCPIVDAGDRVEAGQVIADGPCTDDGEMALGKNLLVAIMPWEGHNYEDAIILSNRL
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                     EDELPAGVNELVRVYVAQKRKISDGDKLAGRHGNKGVIGKILPVEDMPFLADGTPVDI
                     ILNTHGVPRRMNIGQILETHLGWCAHSGWKVDAAKGVPDWAARLPDELLEAQPNAIVS
                     TPVFDGAQEAELQGLLSCTLPNRDGDVLVDADGKAMLFDGRSGEPFPYPVTVGYMYIM
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BASE COUNT      723 a   1173 c   1293 g    664 t
ORIGIN
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  Best Local Similarity   100.0%;  Pred. No. 0.057;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
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Db    2122 TACGGCGTTTCGATGAACCC 2103


RESULT 14
MSGRPOB/c
LOCUS       MSGRPOB                 5084 bp    DNA     linear   BCT 13-SEP-1994
DEFINITION  Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB)
            gene, complete cds and RNA polymerase beta'-subunit rpoC gene,
            partial cds.
ACCESSION   L27989
VERSION     L27989.1  GI:468333
KEYWORDS    RNA polymerase beta-subunit; rpoB gene.
SOURCE      Mycobacterium tuberculosis (strain Rv) DNA.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 5084)
  AUTHORS   Miller,L.P., Crawford,J.T. and Shinnick,T.M.
  TITLE     The rpoB gene of Mycobacterium tuberculosis
  JOURNAL   Antimicrob. Agents Chemother. 38 (4), 805-811 (1994)
  MEDLINE   94304130
FEATURES             Location/Qualifiers
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                     /strain="Rv"
                     /db_xref="taxon:1773"
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            partial cds.
ACCESSION   AF060353
VERSION     AF060353.1  GI:3133464
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 705)
  AUTHORS   Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
            Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
  TITLE     Simultaneous genotyping and species identification using
            hybridization pattern recognition analysis of generic mycobacterium
            DNA arrays
  JOURNAL   Genome Res. 8 (5), 435-448 (1998)
  MEDLINE   98248685
REFERENCE   2  (bases 1 to 705)
  AUTHORS   Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
            Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-APR-1998) Division of Infectious Disease, Affymetrix,
            3380 Central Expressway, Santa Clara, CA 95051, USA
FEATURES             Location/Qualifiers
     source          1. .705
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BASE COUNT      117 a    227 c    250 g    111 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
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Db    331 TACGGCGTTTCGATGAACCC 312


RESULT  10
AR149128/c
LOCUS       AR149128                706 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 24 from patent US 6228575.
ACCESSION   AR149128
VERSION     AR149128.1  GI:15113719
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 706)
  AUTHORS   Gingeras,T.R., Mack,D., Chee,M.S., Berno,A.J., Stryer,L.,
            Ghandour,G. and Wang,C.
  TITLE     Chip-based species identification and phenotypic characterization
            of microorganisms
  JOURNAL   Patent: US 6228575-A 24 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .706
                     /organism="unknown"
BASE COUNT      117 a    227 c    250 g    111 t      1 others
ORIGIN


  Query Match             100.0%;  Score 20;  DB 6;  Length 706;
  Best Local Similarity   100.0%;  Pred. No. 0.054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
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Db    332 TACGGCGTTTCGATGAACCC 313


RESULT  11
I50706/c
LOCUS       I50706                  970 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1 from patent US 5643723.
ACCESSION   I50706
VERSION     I50706.1  GI:2472409
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 970)
  AUTHORS   Persing,D.H., Hunt,J.J., Young,K.K.Y., Felmlee,T.A., Roberts,G.D.
            and Whelan,A.Christian.
  TITLE     Detection of a genetic locus encoding resistance to rifampin in
            mycobacterial cultures and in clinical specimens
  JOURNAL   Patent: US 5643723-A 1 01-JUL-1997;
FEATURES             Location/Qualifiers
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ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.055;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
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Db    671 TACGGCGTTTCGATGAACCC 652


RESULT  12
AX111339/c
LOCUS       AX111339                3534 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 2072 from Patent WO0123604.
ACCESSION   AX111339
VERSION     AX111339.1  GI:13927631
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 3534)
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 2072 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .3534
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                     /strain="Rv"
                     /db_xref="taxon:1773"
BASE COUNT      679 a   1081 c   1188 g    586 t
ORIGIN
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  JOURNAL   Patent: US 5843669-A 136 01-DEC-1998;
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                     /organism="unknown"
BASE COUNT      103 a    201 c    214 g    102 t
ORIGIN
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Qy      1 tacggcgtttcgatgaaccc 20
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Db    296 TACGGCGTTTCGATGAACCC 277
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RESULT   5
AR062058/c
LOCUS       AR062058                620 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 137 from patent US 5843669.
ACCESSION   AR062058
VERSION     AR062058.1  GI:5989749
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
  TITLE     Cleavage of nucleic acid acid using thermostable methoanococcus
            jannaschii FEN-1 endonucleases
  JOURNAL   Patent: US 5843669-A 137 01-DEC-1998;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
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ORIGIN
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  Best Local Similarity   100.0%;  Pred. No. 0.054;
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Qy      1 tacggcgtttcgatgaaccc 20
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Db    296 TACGGCGTTTCGATGAACCC 277
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RESULT   6
AR062059
LOCUS       AR062059                620 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 138 from patent US 5843669.
ACCESSION   AR062059
VERSION     AR062059.1  GI:5989750
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
  TITLE     Cleavage of nucleic acid acid using thermostable methoanococcus
            jannaschii FEN-1 endonucleases
  JOURNAL   Patent: US 5843669-A 138 01-DEC-1998;
FEATURES             Location/Qualifiers
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  Best Local Similarity   100.0%;  Pred. No. 0.054;
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Qy      1 tacggcgtttcgatgaaccc 20
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Db    325 TACGGCGTTTCGATGAACCC 344
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RESULT   7
AR062060
LOCUS       AR062060                620 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 139 from patent US 5843669.
ACCESSION   AR062060
VERSION     AR062060.1  GI:5989751
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
  TITLE     Cleavage of nucleic acid acid using thermostable methoanococcus
            jannaschii FEN-1 endonucleases
  JOURNAL   Patent: US 5843669-A 139 01-DEC-1998;
FEATURES             Location/Qualifiers
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BASE COUNT      102 a    214 c    201 g    103 t
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Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    325 TACGGCGTTTCGATGAACCC 344
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RESULT   8
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LOCUS       AR062061                620 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 140 from patent US 5843669.
ACCESSION   AR062061
VERSION     AR062061.1  GI:5989752
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
  TITLE     Cleavage of nucleic acid acid using thermostable methoanococcus
            jannaschii FEN-1 endonucleases
  JOURNAL   Patent: US 5843669-A 140 01-DEC-1998;
FEATURES             Location/Qualifiers
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  Best Local Similarity   100.0%;  Pred. No. 0.054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    325 TACGGCGTTTCGATGAACCC 344
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RESULT   9
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                mutation 234 G"
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                /replace="c"
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                /replace="t"
     variation  254
                /phenotype="rifampicin resistant"
                /replace="c"
BASE COUNT       77 a    140 c    148 g     67 t
ORIGIN


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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    428 TACGGCGTTTCGATGAACCC 409


RESULT   2
AR067448/c
LOCUS       AR067448                 432 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 59 from patent US 5851763.
ACCESSION   AR067448
VERSION     AR067448.1  GI:5998670
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 432)
  AUTHORS   Heym,B., Cole,S., Young,D., Zhang,Y., Honore,N., Telenti,A. and
            Bodmer,T.
  TITLE     Rapid detection of antibiotic resistance in mycobacterium
            tuberculosis
  JOURNAL   Patent: US 5851763-A 59 22-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .432
                     /organism="unknown"
BASE COUNT       77 a    139 c    149 g     67 t
ORIGIN


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  Best Local Similarity  100.0%;  Pred. No. 0.053;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    428 TACGGCGTTTCGATGAACCC 409


RESULT   3
AR062056/c
LOCUS       AR062056                 620 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 135 from patent US 5843669.
ACCESSION   AR062056
VERSION     AR062056.1  GI:5989747
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
  TITLE     Cleavage of nucleic acid acid using thermostable methoanococcus
            jannaschii FEN-1 endonucleases
  JOURNAL   Patent: US 5843669-A 135 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .620
                     /organism="unknown"
BASE COUNT      103 a    202 c    214 g    101 t
ORIGIN


  Query Match           100.0%;  Score 20;  DB 6;  Length 620;
  Best Local Similarity  100.0%;  Pred. No. 0.054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    296 TACGGCGTTTCGATGAACCC 277


RESULT   4
AR062057/c
LOCUS       AR062057                 620 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 136 from patent US 5843669.
ACCESSION   AR062057
VERSION     AR062057.1  GI:5989748
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
  TITLE     Cleavage of nucleic acid acid using thermostable methoanococcus
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:49:01 ; Search time 2179.67 Seconds
(without alignments)
192.016 Million cell updates/sec

Title: US-09-786-105-2
Perfect score: 20
Sequence: 1 tacggcgtttcgatgaaccc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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16: em_fun:*
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30: em_htg_hum:*
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33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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c 2	20	100.0	432	6	AR067448	AR067448 Sequence
c 3	20	100.0	620	6	AR062056	AR062056 Sequence
c 4	20	100.0	620	6	AR062057	AR062057 Sequence
c 5	20	100.0	620	6	AR062058	AR062058 Sequence
6	20	100.0	620	6	AR062059	AR062059 Sequence
7	20	100.0	620	6	AR062060	AR062060 Sequence
8	20	100.0	620	6	AR062061	AR062061 Sequence
c 9	20	100.0	705	1	AF060353	AF060353 Mycobacte
c 10	20	100.0	706	6	AR149128	AR149128 Sequence
c 11	20	100.0	970	6	I50706	I50706 Sequence 1
c 12	20	100.0	3534	6	AX111339	AX111339 Sequence
c 13	20	100.0	3853	1	MTU12205	U12205 Mycobacteri
c 14	20	100.0	5084	1	MSGRPOB	L27989 Mycobacteri
c 15	20	100.0	19352	1	AE006964	AE006964 Mycobacte
c 16	20	100.0	19770	1	MTCI376	Z95972 Mycobacteri
c 17	17	85.0	3316	1	AF172323	AF172323 Bacillus
18	15	75.0	27	6	I50714	I50714 Sequence 9
c 19	15	75.0	11843	1	AE008100	AE008100 Agrobacte
c 20	15	75.0	13735	1	AE009134	AE009134 Agrobacte
21	15	75.0	239050	1	AL596169	AL596169 Listeria
22	14	70.0	143	3	AF277396	AF277396 Crithidia
23	14	70.0	409	1	CSPAG22R	Z47191 Calothrix D
24	14	70.0	442	8	AF080428	AF080428 Agrocybe
25	14	70.0	458	8	AF080421	AF080421 Agrocybe
26	14	70.0	518	1	AF325874	AF325874 Staphyloc
27	14	70.0	762	1	SHFENTC	M63306 S.flexneri
28	14	70.0	791	33	AC048639	Ac048639 Giardia i
29	14	70.0	1128	8	AB044172	AB044172 Yamagishi
c 30	14	70.0	1194	3	FHEFHMDA	L36247 Fasciola he
31	14	70.0	1959	8	ATHTUBA6A	M84699 Arabidopsis
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33	14	70.0	2615	10	RNPKCETA	X68400 R.norvegicu
34	14	70.0	3218	10	AF146518	AF146518 Rattus no
35	14	70.0	3240	8	SCU06465	U06465 Saccharomyc
c 36	14	70.0	3447	6	AR067447	AR067447 Sequence
37	14	70.0	3639	10	AF214568	AF214568 Rattus no
38	14	70.0	4075	10	AF146044	AF146044 Rattus no
39	14	70.0	4887	3	AY069181	AY069181 Drosophil
40	14	70.0	6211	3	CEF14A5	Z75951 Caenorhabdi
41	14	70.0	6275	6	AX345453	AX345453 Sequence
42	14	70.0	6275	6	AX348335	AX348335 Sequence
c 43	14	70.0	9086	1	AE001767	AE001767 Thermotog
44	14	70.0	9728	6	AX346805	AX346805 Sequence
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ALIGNMENTS

RESULT 1
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LOCUS MSGRIFRNAP 432 bp DNA linear BCT 21-MAY-1993
DEFINITION Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin resistance gene, complete cds.
ACCESSION L05910
VERSION L05910.1 GI:149991
KEYWORDS RNA polymerase beta-subunit; rifampicin resistance.
SOURCE Mycobacterium tuberculosis (strain H37) DNA.
ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 432)
AUTHORS Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T., Colston,J., Matter,L., Schopfer,K. and Bodmer,T.
TITLE Detection of rifampicin-resistance mutation in Mycobacterium tuberculosis
JOURNAL Antimicrob. Agents Chemother. 341, 647-650 (1993)
FEATURES Location/Qualifiers
source 1. .432
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:54:21 ; Search time 146.61 Seconds
(without alignments)
33.508 Million cell updates/sec

Title: US-09-786-105-3
Perfect score: 20
Sequence: 1 tacggtcggcgagctgatcc 20

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Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	4	US-08-750-088A-70	Sequence 70, Appl
2	20	100.0	306	4	US-09-147-935A-2	Sequence 2, Appli
3	20	100.0	306	4	US-09-147-935A-6	Sequence 6, Appli
4	20	100.0	306	4	US-09-147-935A-7	Sequence 7, Appli
5	20	100.0	306	4	US-09-147-935A-41	Sequence 41, Appl
6	20	100.0	306	4	US-09-147-935A-50	Sequence 50, Appl
7	20	100.0	432	2	US-08-313-185-59	Sequence 59, Appl
8	20	100.0	432	3	US-09-082-614A-59	Sequence 59, Appl
9	20	100.0	970	1	US-08-250-030-1	Sequence 1, Appli
10	20	100.0	970	5	PCT-US95-06790-1	Sequence 1, Appli
11	19	95.0	306	4	US-09-147-935A-44	Sequence 44, Appl
12	18.4	92.0	25	4	US-08-750-088A-30	Sequence 30, Appl
13	18.4	92.0	306	4	US-09-147-935A-4	Sequence 4, Appli
14	18.4	92.0	306	4	US-09-147-935A-9	Sequence 9, Appli
15	18.4	92.0	306	4	US-09-147-935A-10	Sequence 10, Appl
16	18.4	92.0	306	4	US-09-147-935A-20	Sequence 20, Appl
17	18.4	92.0	306	4	US-09-147-935A-23	Sequence 23, Appl
18	18.4	92.0	306	4	US-09-147-935A-45	Sequence 45, Appl
19	17.4	87.0	306	4	US-09-147-935A-13	Sequence 13, Appl
20	17.4	87.0	306	4	US-09-147-935A-16	Sequence 16, Appl
21	17.4	87.0	306	4	US-09-147-935A-25	Sequence 25, Appl
22	17.4	87.0	306	4	US-09-147-935A-31	Sequence 31, Appl
23	17.4	87.0	306	4	US-09-147-935A-39	Sequence 39, Appl
24	17.4	87.0	306	4	US-09-147-935A-43	Sequence 43, Appl
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28	16.8	84.0	306	4	US-09-147-935A-8	Sequence 8, Appli
29	15.8	79.0	306	4	US-09-147-935A-5	Sequence 5, Appli
30	15.8	79.0	306	4	US-09-147-935A-12	Sequence 12, Appl
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34	15.8	79.0	306	4	US-09-147-935A-18	Sequence 18, Appl
35	15.8	79.0	306	4	US-09-147-935A-19	Sequence 19, Appl
36	15.8	79.0	306	4	US-09-147-935A-21	Sequence 21, Appl
37	15.8	79.0	306	4	US-09-147-935A-24	Sequence 24, Appl
38	15.8	79.0	306	4	US-09-147-935A-26	Sequence 26, Appl
39	15.8	79.0	306	4	US-09-147-935A-29	Sequence 29, Appl
40	15.8	79.0	306	4	US-09-147-935A-30	Sequence 30, Appl
41	15.8	79.0	306	4	US-09-147-935A-32	Sequence 32, Appl
42	15.8	79.0	306	4	US-09-147-935A-34	Sequence 34, Appl
43	15.8	79.0	306	4	US-09-147-935A-35	Sequence 35, Appl
44	15.8	79.0	306	4	US-09-147-935A-36	Sequence 36, Appl
45	15.8	79.0	306	4	US-09-147-935A-38	Sequence 38, Appl

ALIGNMENTS

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RESULT   1
US-08-750-088A-70
; Sequence 70, Application US/08750088A
; Patent No. 6329138
;  GENERAL INFORMATION:
;    APPLICANT:  DE BEENHOUWER, HANS
;    APPLICANT:  PORTAELS, FRAN OISE
;    APPLICANT:  MACHTELINCKX, LIEVE
;    APPLICANT:  JANNES, GEERT
;    APPLICANT:  ROSSAU, RUDI
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF THE ANTIBIOTIC
;    TITLE OF INVENTION:  RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  US
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/750,088A
;      FILING DATE:  21-FEB-1997
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GOLDSTEIN, JORGE A.
;      REGISTRATION NUMBER:  29,021
;      REFERENCE/DOCKET NUMBER:  1657.0010000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  70:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-750-088A-70


  Query Match           100.0%;  Score 20;  DB 4;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0.23;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Db      1 TACGGTCGGCGAGCTGATCC 20


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; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
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;   ORGANISM: Mycobacterium africanum
US-09-147-935A-2


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Db      5 tacggtcggcgagctgatcc 24


RESULT   3
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; Sequence 6, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 6
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium bovis
US-09-147-935A-6


  Query Match             100.0%;  Score 20;  DB 4;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 tacggtcggcgagctgatcc 24


RESULT   4
US-09-147-935A-7
; Sequence 7, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 7
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium bovis BCG
US-09-147-935A-7


  Query Match             100.0%;  Score 20;  DB 4;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 tacggtcggcgagctgatcc 24


RESULT   5
US-09-147-935A-41
; Sequence 41, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 41
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-41


  Query Match             100.0%;  Score 20;  DB 4;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 tacggtcggcgagctgatcc 24


RESULT   6
US-09-147-935A-50
; Sequence 50, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
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;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 50
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-50


  Query Match             100.0%;  Score 20;  DB 4;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 tacggtcggcgagctgatcc 24


RESULT   7
US-08-313-185-59
; Sequence 59, Application US/08313185
; Patent No. 5851763
;  GENERAL INFORMATION:
;    APPLICANT:  Heym, Beate
;    APPLICANT:  Cole, Stewart
;    APPLICANT:  Young, Douglas
;    APPLICANT:  Zhang, Ying
;    APPLICANT:  Honore, Nadine
;    APPLICANT:  Telenti, Amalio
;    APPLICANT:  Bodmer, Thomas
;    TITLE OF INVENTION:  Rapid Detection of Antibiotic Resistance
;    TITLE OF INVENTION:  in Mycobacterium Tuberculosis
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/313,185
;      FILING DATE:  12-OCT-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  02356.0068-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-313-185-59


  Query Match             100.0%;  Score 20;  DB 2;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 0.25;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db     18 TACGGTCGGCGAGCTGATCC 37


RESULT   8
US-09-082-614A-59
; Sequence 59, Application US/09082614A
; Patent No. 6124098
;  GENERAL INFORMATION:
;    APPLICANT:  Heym, Beate
;    APPLICANT:  Cole, Stewart
;    APPLICANT:  Young, Douglas
;    APPLICANT:  Zhang, Ying
;    APPLICANT:  Honore, Nadine
;    APPLICANT:  Telenti, Amalio
;    APPLICANT:  Bodmer, Thomas
;    TITLE OF INVENTION:  Rapid Detection of Antibiotic Resistance
;    TITLE OF INVENTION:  in Mycobacterium Tuberculosis
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/082,614A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/313,185
;      FILING DATE:  12-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  02356.0068-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-082-614A-59


  Query Match             100.0%;  Score 20;  DB 3;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 0.25;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db     18 TACGGTCGGCGAGCTGATCC 37


RESULT   9
US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
;  GENERAL INFORMATION:
;    APPLICANT:  Persing, David H.
;    TITLE OF INVENTION:  Detection of a Genetic Locus Encoding
;    TITLE OF INVENTION:  Resistance to Rifampin in Mycobacterial Cultures and in
```

```
;    TITLE OF INVENTION:  Clinical Specimens
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schwegman, Lundberg & Woessner
;      STREET:  3500 IDS Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/250,030
;      FILING DATE:  26-MAY-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueting, Ann M.
;      REGISTRATION NUMBER:  33,977
;      REFERENCE/DOCKET NUMBER:  150.105US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-339-0331
;      TELEFAX:  612-339-3061
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  970 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-250-030-1


  Query Match             100.0%;  Score 20;  DB 1;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 0.25;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggtcggcgagctgatcc 20
           ||||||||||||||||||||
Db     261 TACGGTCGGCGAGCTGATCC 280


RESULT  10
PCT-US95-06790-1
; Sequence 1, Application PC/TUS9506790
;  GENERAL INFORMATION:
;    APPLICANT:  Mayo Foundation for Medical Education and Research
;    APPLICANT:  and Hoffmann-La Roche Inc.
;    TITLE OF INVENTION:  Detection of a Genetic Locus Encoding
;    TITLE OF INVENTION:  Resistance to Rifampin
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schwegman, Lundberg & Woessner
;      STREET:  3500 IDS Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/06790
;      FILING DATE:  26-MAY-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Raasch, Kevin W.
;      REGISTRATION NUMBER:  35,651
;      REFERENCE/DOCKET NUMBER:  150.105WO1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-339-0331
;      TELEFAX:  612-339-3061
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  970 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
PCT-US95-06790-1


  Query Match             100.0%;  Score 20;  DB 5;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 0.25;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggtcggcgagctgatcc 20
           ||||||||||||||||||||
Db     261 TACGGTCGGCGAGCTGATCC 280


RESULT  11
US-09-147-935A-44
; Sequence 44, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:  A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:  50
;  SOFTWARE:  KOPATIN 1.0
; SEQ ID NO 44
;  LENGTH: 306
;  TYPE: DNA
;  ORGANISM: Mycobacterium xenopi
US-09-147-935A-44


  Query Match             95.0%;  Score 19;  DB 4;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 0.75;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 acggtcggcgagctgatcc 20
           ||||||||||||||||||||
Db       6 acggtcggcgagctgatcc 24


RESULT  12
US-08-750-088A-30
; Sequence 30, Application US/08750088A
; Patent No. 6329138
;  GENERAL INFORMATION:
;    APPLICANT:  DE BEENHOUWER, HANS
;    APPLICANT:  PORTAELS, FRAN OISE
;    APPLICANT:  MACHTELINCKX, LIEVE
;    APPLICANT:  JANNES, GEERT
;    APPLICANT:  ROSSAU, RUDI
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF THE ANTIBIOTIC
;    TITLE OF INVENTION:  RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  US
```

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;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/750,088A
;      FILING DATE:  21-FEB-1997
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GOLDSTEIN, JORGE A.
;      REGISTRATION NUMBER:  29,021
;      REFERENCE/DOCKET NUMBER:  1657.0010000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  25 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-750-088A-30


  Query Match             92.0%;  Score 18.4;  DB 4;  Length 25;
  Best Local Similarity   95.0%;  Pred. No. 1.4;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          | ||||||||||||||||||
Db      6 TTCGGTCGGCGAGCTGATCC 25


RESULT  13
US-09-147-935A-4
; Sequence 4, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 4
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium aurum
US-09-147-935A-4


  Query Match             92.0%;  Score 18.4;  DB 4;  Length 306;
  Best Local Similarity   95.0%;  Pred. No. 1.5;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||| ||||||||||||||||
Db      5 taccgtcggcgagctgatcc 24


RESULT  14
US-09-147-935A-9
; Sequence 9, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 9
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium celatum Type2
US-09-147-935A-9


  Query Match             92.0%;  Score 18.4;  DB 4;  Length 306;
  Best Local Similarity   95.0%;  Pred. No. 1.5;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||| ||||||||||||||||
Db      5 taccgtcggcgagctgatcc 24


RESULT  15
US-09-147-935A-10
; Sequence 10, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 10
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium chelonae
US-09-147-935A-10


  Query Match             92.0%;  Score 18.4;  DB 4;  Length 306;
  Best Local Similarity   95.0%;  Pred. No. 1.5;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||| ||||||||||||||||
Db      5 taccgtcggcgagctgatcc 24


Search completed: August  7, 2002, 21:54:21
Job time: 24016 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:52:14 ; Search time 147.68 Seconds
(without alignments)
33.266 Million cell updates/sec

Title: US-09-786-105-1
Perfect score: 20
Sequence: 1 tacggtcggcgagctgatcc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

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Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	4	US-08-750-088A-70	Sequence 70, Appl
2	20	100.0	306	4	US-09-147-935A-2	Sequence 2, Appli
3	20	100.0	306	4	US-09-147-935A-6	Sequence 6, Appli
4	20	100.0	306	4	US-09-147-935A-7	Sequence 7, Appli
5	20	100.0	306	4	US-09-147-935A-41	Sequence 41, Appl
6	20	100.0	306	4	US-09-147-935A-50	Sequence 50, Appl
7	20	100.0	432	2	US-08-313-185-59	Sequence 59, Appl
8	20	100.0	432	3	US-09-082-614A-59	Sequence 59, Appl
9	20	100.0	970	1	US-08-250-030-1	Sequence 1, Appli
10	20	100.0	970	5	PCT-US95-06790-1	Sequence 1, Appli
11	19	95.0	306	4	US-09-147-935A-44	Sequence 44, Appl
12	18	90.0	25	4	US-08-750-088A-30	Sequence 30, Appl
13	16	80.0	306	4	US-09-147-935A-4	Sequence 4, Appli
14	16	80.0	306	4	US-09-147-935A-9	Sequence 9, Appli
15	16	80.0	306	4	US-09-147-935A-10	Sequence 10, Appl
16	16	80.0	306	4	US-09-147-935A-13	Sequence 13, Appl
17	16	80.0	306	4	US-09-147-935A-20	Sequence 20, Appl
18	16	80.0	306	4	US-09-147-935A-23	Sequence 23, Appl
19	16	80.0	306	4	US-09-147-935A-31	Sequence 31, Appl
20	16	80.0	306	4	US-09-147-935A-39	Sequence 39, Appl
21	16	80.0	306	4	US-09-147-935A-45	Sequence 45, Appl
22	15	75.0	4403765	4	US-09-103-840A-2	Sequence 2, Appli
23	15	75.0	4411529	4	US-09-103-840A-1	Sequence 1, Appli
24	14	70.0	50	1	US-08-672-158A-10	Sequence 10, Appl
25	14	70.0	306	4	US-09-147-935A-1	Sequence 1, Appli
26	14	70.0	490	1	US-08-133-711-43	Sequence 43, Appl
c 27	14	70.0	6822	4	US-09-426-998-3	Sequence 3, Appli
c 28	14	70.0	7741	4	US-09-426-998-4	Sequence 4, Appli
29	13	65.0	279	1	US-07-612-674-11	Sequence 11, Appl
30	13	65.0	306	4	US-09-147-935A-12	Sequence 12, Appl
31	13	65.0	306	4	US-09-147-935A-14	Sequence 14, Appl
32	13	65.0	306	4	US-09-147-935A-15	Sequence 15, Appl
33	13	65.0	306	4	US-09-147-935A-16	Sequence 16, Appl
34	13	65.0	306	4	US-09-147-935A-18	Sequence 18, Appl
35	13	65.0	306	4	US-09-147-935A-47	Sequence 47, Appl
c 36	13	65.0	408	4	US-09-199-637A-222	Sequence 222, App
c 37	13	65.0	663	1	US-08-506-404D-1	Sequence 1, Appli
c 38	13	65.0	663	3	US-09-035-754-1	Sequence 1, Appli
c 39	13	65.0	720	3	US-09-094-359-3	Sequence 3, Appli
c 40	13	65.0	720	3	US-09-094-359-5	Sequence 5, Appli
c 41	13	65.0	720	3	US-09-094-359-7	Sequence 7, Appli
c 42	13	65.0	720	3	US-09-094-359-9	Sequence 9, Appli
c 43	13	65.0	720	3	US-09-172-063-11	Sequence 11, Appl
c 44	13	65.0	720	3	US-09-172-063-12	Sequence 12, Appl
c 45	13	65.0	720	3	US-09-172-063-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-750-088A-70
; Sequence 70, Application US/08750088A
; Patent No. 6329138
; GENERAL INFORMATION:
; APPLICANT: DE BEENHOUWER, HANS
; APPLICANT: PORTAELS, FRAN OISE
; APPLICANT: MACHTELINCKX, LIEVE
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
; TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,088A
; FILING DATE: 21-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDSTEIN, JORGE A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 1657.0010000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-750-088A-70

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      1 TACGGTCGGCGAGCTGATCC 20


RESULT   2
US-09-147-935A-2
; Sequence 2, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 2
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium africanum
US-09-147-935A-2


  Query Match            100.0%;  Score 20;  DB 4;  Length 306;
  Best Local Similarity  100.0%;  Pred. No. 0.0022;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 tacggtcggcgagctgatcc 24


RESULT   3
US-09-147-935A-6
; Sequence 6, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 6
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium bovis
US-09-147-935A-6


  Query Match            100.0%;  Score 20;  DB 4;  Length 306;
  Best Local Similarity  100.0%;  Pred. No. 0.0022;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 tacggtcggcgagctgatcc 24


RESULT   4
US-09-147-935A-7
; Sequence 7, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 7
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium bovis BCG
US-09-147-935A-7


  Query Match            100.0%;  Score 20;  DB 4;  Length 306;
  Best Local Similarity  100.0%;  Pred. No. 0.0022;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 tacggtcggcgagctgatcc 24


RESULT   5
US-09-147-935A-41
; Sequence 41, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 41
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-41


  Query Match            100.0%;  Score 20;  DB 4;  Length 306;
  Best Local Similarity  100.0%;  Pred. No. 0.0022;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 tacggtcggcgagctgatcc 24


RESULT   6
US-09-147-935A-50
; Sequence 50, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
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;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 50
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-50


  Query Match            100.0%;  Score 20;  DB 4;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 0.0022;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 tacggtcggcgagctgatcc 24


RESULT   7
US-08-313-185-59
; Sequence 59, Application US/08313185
; Patent No. 5851763
;  GENERAL INFORMATION:
;    APPLICANT:  Heym, Beate
;    APPLICANT:  Cole, Stewart
;    APPLICANT:  Young, Douglas
;    APPLICANT:  Zhang, Ying
;    APPLICANT:  Honore, Nadine
;    APPLICANT:  Telenti, Amalio
;    APPLICANT:  Bodmer, Thomas
;    TITLE OF INVENTION:  Rapid Detection of Antibiotic Resistance
;    TITLE OF INVENTION:  in Mycobacterium Tuberculosis
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/313,185
;      FILING DATE:  12-OCT-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  02356.0068-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-313-185-59


  Query Match            100.0%;  Score 20;  DB 2;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 0.0022;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db     18 TACGGTCGGCGAGCTGATCC 37


RESULT   8
US-09-082-614A-59
; Sequence 59, Application US/09082614A
; Patent No. 6124098
;  GENERAL INFORMATION:
;    APPLICANT:  Heym, Beate
;    APPLICANT:  Cole, Stewart
;    APPLICANT:  Young, Douglas
;    APPLICANT:  Zhang, Ying
;    APPLICANT:  Honore, Nadine
;    APPLICANT:  Telenti, Amalio
;    APPLICANT:  Bodmer, Thomas
;    TITLE OF INVENTION:  Rapid Detection of Antibiotic Resistance
;    TITLE OF INVENTION:  in Mycobacterium Tuberculosis
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/082,614A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/313,185
;      FILING DATE:  12-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  02356.0068-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-082-614A-59


  Query Match            100.0%;  Score 20;  DB 3;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 0.0022;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db     18 TACGGTCGGCGAGCTGATCC 37


RESULT   9
US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
;  GENERAL INFORMATION:
;    APPLICANT:  Persing, David H.
;    TITLE OF INVENTION:  Detection of a Genetic Locus Encoding
;    TITLE OF INVENTION:  Resistance to Rifampin in Mycobacterial Cultures and in
```

```
;    TITLE OF INVENTION:  Clinical Specimens
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schwegman, Lundberg & Woessner
;      STREET:  3500 IDS Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/250,030
;      FILING DATE:  26-MAY-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueting, Ann M.
;      REGISTRATION NUMBER:  33,977
;      REFERENCE/DOCKET NUMBER:  150.105US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-339-0331
;      TELEFAX:  612-339-3061
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  970 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-250-030-1


  Query Match             100.0%;  Score 20;  DB 1;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 0.0021;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggtcggcgagctgatcc 20
           ||||||||||||||||||||
Db     261 TACGGTCGGCGAGCTGATCC 280


RESULT  10
PCT-US95-06790-1
; Sequence 1, Application PC/TUS9506790
;  GENERAL INFORMATION:
;    APPLICANT:  Mayo Foundation for Medical Education and Research
;    APPLICANT:  and Hoffmann-La Roche Inc.
;    TITLE OF INVENTION:  Detection of a Genetic Locus Encoding
;    TITLE OF INVENTION:  Resistance to Rifampin
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schwegman, Lundberg & Woessner
;      STREET:  3500 IDS Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/06790
;      FILING DATE:  26-MAY-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Raasch, Kevin W.
;      REGISTRATION NUMBER:  35,651
;      REFERENCE/DOCKET NUMBER:  150.105WO1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-339-0331
;      TELEFAX:  612-339-3061
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  970 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
PCT-US95-06790-1


  Query Match             100.0%;  Score 20;  DB 5;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 0.0021;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggtcggcgagctgatcc 20
           ||||||||||||||||||||
Db     261 TACGGTCGGCGAGCTGATCC 280


RESULT  11
US-09-147-935A-44
; Sequence 44, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:  A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:  50
;  SOFTWARE:  KOPATIN 1.0
; SEQ ID NO 44
;  LENGTH: 306
;  TYPE: DNA
;  ORGANISM: Mycobacterium xenopi
US-09-147-935A-44


  Query Match              95.0%;  Score 19;  DB 4;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 0.0084;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 acggtcggcgagctgatcc 20
           ||||||||||||||||||||
Db       6 acggtcggcgagctgatcc 24


RESULT  12
US-08-750-088A-30
; Sequence 30, Application US/08750088A
; Patent No. 6329138
;  GENERAL INFORMATION:
;    APPLICANT:  DE BEENHOUWER, HANS
;    APPLICANT:  PORTAELS, FRAN OISE
;    APPLICANT:  MACHTELINCKX, LIEVE
;    APPLICANT:  JANNES, GEERT
;    APPLICANT:  ROSSAU, RUDI
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF THE ANTIBIOTIC
;    TITLE OF INVENTION:  RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  US
```

```
;    TITLE OF INVENTION: Clinical Specimens
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schwegman, Lundberg & Woessner
;      STREET:  3500 IDS Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/250,030
;      FILING DATE:  26-MAY-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueting, Ann M.
;      REGISTRATION NUMBER:  33,977
;      REFERENCE/DOCKET NUMBER:  150.105US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-339-0331
;      TELEFAX:  612-339-3061
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  970 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-250-030-1


  Query Match           100.0%;  Score 20;  DB 1;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 0.0021;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggtcggcgagctgatcc 20
           ||||||||||||||||||||
Db     261 TACGGTCGGCGAGCTGATCC 280


RESULT  10
PCT-US95-06790-1
; Sequence 1, Application PC/TUS9506790
;  GENERAL INFORMATION:
;    APPLICANT:  Mayo Foundation for Medical Education and Research
;    APPLICANT:  and Hoffmann-La Roche Inc.
;    TITLE OF INVENTION:  Detection of a Genetic Locus Encoding
;    TITLE OF INVENTION:  Resistance to Rifampin
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schwegman, Lundberg & Woessner
;      STREET:  3500 IDS Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/06790
;      FILING DATE:  26-MAY-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Raasch, Kevin W.
;      REGISTRATION NUMBER:  35,651
;      REFERENCE/DOCKET NUMBER:  150.105WO1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-339-0331
;      TELEFAX:  612-339-3061
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  970 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
PCT-US95-06790-1


  Query Match           100.0%;  Score 20;  DB 5;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 0.0021;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggtcggcgagctgatcc 20
           ||||||||||||||||||||
Db     261 TACGGTCGGCGAGCTGATCC 280


RESULT  11
US-09-147-935A-44
; Sequence 44, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:  A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:  50
;  SOFTWARE:  KOPATIN 1.0
; SEQ ID NO 44
;  LENGTH: 306
;  TYPE: DNA
;  ORGANISM: Mycobacterium xenopi
US-09-147-935A-44


  Query Match           95.0%;  Score 19;  DB 4;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 0.0084;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 acggtcggcgagctgatcc 20
           ||||||||||||||||||||
Db       6 acggtcggcgagctgatcc 24


RESULT  12
US-08-750-088A-30
; Sequence 30, Application US/08750088A
; Patent No. 6329138
;  GENERAL INFORMATION:
;    APPLICANT:  DE BEENHOUWER, HANS
;    APPLICANT:  PORTAELS, FRAN OISE
;    APPLICANT:  MACHTELINCKX, LIEVE
;    APPLICANT:  JANNES, GEERT
;    APPLICANT:  ROSSAU, RUDI
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF THE ANTIBIOTIC
;    TITLE OF INVENTION:  RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  US
```

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;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 50
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-50


  Query Match            100.0%;  Score 20;  DB 4;  Length 306;
  Best Local Similarity  100.0%;  Pred. No. 0.0022;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 tacggtcggcgagctgatcc 24


RESULT   7
US-08-313-185-59
; Sequence 59, Application US/08313185
; Patent No. 5851763
;  GENERAL INFORMATION:
;    APPLICANT:  Heym, Beate
;    APPLICANT:  Cole, Stewart
;    APPLICANT:  Young, Douglas
;    APPLICANT:  Zhang, Ying
;    APPLICANT:  Honore, Nadine
;    APPLICANT:  Telenti, Amalio
;    APPLICANT:  Bodmer, Thomas
;    TITLE OF INVENTION:  Rapid Detection of Antibiotic Resistance
;    TITLE OF INVENTION:  in Mycobacterium Tuberculosis
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/313,185
;      FILING DATE:  12-OCT-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  02356.0068-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-313-185-59


  Query Match            100.0%;  Score 20;  DB 2;  Length 432;
  Best Local Similarity  100.0%;  Pred. No. 0.0022;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db     18 TACGGTCGGCGAGCTGATCC 37


RESULT   8
US-09-082-614A-59
; Sequence 59, Application US/09082614A
; Patent No. 6124098
;  GENERAL INFORMATION:
;    APPLICANT:  Heym, Beate
;    APPLICANT:  Cole, Stewart
;    APPLICANT:  Young, Douglas
;    APPLICANT:  Zhang, Ying
;    APPLICANT:  Honore, Nadine
;    APPLICANT:  Telenti, Amalio
;    APPLICANT:  Bodmer, Thomas
;    TITLE OF INVENTION:  Rapid Detection of Antibiotic Resistance
;    TITLE OF INVENTION:  in Mycobacterium Tuberculosis
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/082,614A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/313,185
;      FILING DATE:  12-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  02356.0068-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-082-614A-59


  Query Match            100.0%;  Score 20;  DB 3;  Length 432;
  Best Local Similarity  100.0%;  Pred. No. 0.0022;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db     18 TACGGTCGGCGAGCTGATCC 37


RESULT   9
US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
;  GENERAL INFORMATION:
;    APPLICANT:  Persing, David H.
;    TITLE OF INVENTION:  Detection of a Genetic Locus Encoding
;    TITLE OF INVENTION:  Resistance to Rifampin in Mycobacterial Cultures and
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;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/750,088A
;      FILING DATE:  21-FEB-1997
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GOLDSTEIN, JORGE A.
;      REGISTRATION NUMBER:  29,021
;      REFERENCE/DOCKET NUMBER:  1657.0010000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  25 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-750-088A-30


  Query Match             90.0%;  Score 18;  DB 4;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 0.038;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 cggtcggcgagctgatcc 20
          ||||||||||||||||||
Db      8 CGGTCGGCGAGCTGATCC 25


RESULT  13
US-09-147-935A-4
; Sequence 4, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 4
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium aurum
US-09-147-935A-4


  Query Match             80.0%;  Score 16;  DB 4;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 0.46;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 gtcggcgagctgatcc 20
          ||||||||||||||||
Db      9 gtcggcgagctgatcc 24


RESULT  14
US-09-147-935A-9
; Sequence 9, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 9
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium celatum Type2
US-09-147-935A-9


  Query Match             80.0%;  Score 16;  DB 4;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 0.46;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 gtcggcgagctgatcc 20
          ||||||||||||||||
Db      9 gtcggcgagctgatcc 24


RESULT  15
US-09-147-935A-10
; Sequence 10, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 10
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium chelonae
US-09-147-935A-10


  Query Match             80.0%;  Score 16;  DB 4;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 0.46;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 gtcggcgagctgatcc 20
          ||||||||||||||||
Db      9 gtcggcgagctgatcc 24


Search completed: August  7, 2002, 23:51:45
Job time: 7171 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:51:48 ; Search time 147.68 Seconds
(without alignments)
33.266 Million cell updates/sec

Title: US-09-786-105-3
Perfect score: 20
Sequence: 1 tacggtcggcgagctgatcc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	4	US-08-750-088A-70	Sequence 70, Appl
	2	20	100.0	306	4	US-09-147-935A-2	Sequence 2, Appli
	3	20	100.0	306	4	US-09-147-935A-6	Sequence 6, Appli
	4	20	100.0	306	4	US-09-147-935A-7	Sequence 7, Appli
	5	20	100.0	306	4	US-09-147-935A-41	Sequence 41, Appl
	6	20	100.0	306	4	US-09-147-935A-50	Sequence 50, Appl
	7	20	100.0	432	2	US-08-313-185-59	Sequence 59, Appl
	8	20	100.0	432	3	US-09-082-614A-59	Sequence 59, Appl
	9	20	100.0	970	1	US-08-250-030-1	Sequence 1, Appli
	10	20	100.0	970	5	PCT-US95-06790-1	Sequence 1, Appli
	11	19	95.0	306	4	US-09-147-935A-44	Sequence 44, Appl
	12	18	90.0	25	4	US-08-750-088A-30	Sequence 30, Appl
	13	16	80.0	306	4	US-09-147-935A-4	Sequence 4, Appli
	14	16	80.0	306	4	US-09-147-935A-9	Sequence 9, Appli
	15	16	80.0	306	4	US-09-147-935A-10	Sequence 10, Appl
	16	16	80.0	306	4	US-09-147-935A-13	Sequence 13, Appl
	17	16	80.0	306	4	US-09-147-935A-20	Sequence 20, Appl
	18	16	80.0	306	4	US-09-147-935A-23	Sequence 23, Appl
	19	16	80.0	306	4	US-09-147-935A-31	Sequence 31, Appl
	20	16	80.0	306	4	US-09-147-935A-39	Sequence 39, Appl
	21	16	80.0	306	4	US-09-147-935A-45	Sequence 45, Appl
	22	15	75.0	4403765	4	US-09-103-840A-2	Sequence 2, Appli
	23	15	75.0	4411529	4	US-09-103-840A-1	Sequence 1, Appli
	24	14	70.0	50	1	US-08-672-158A-10	Sequence 10, Appl
	25	14	70.0	306	4	US-09-147-935A-1	Sequence 1, Appli
	26	14	70.0	490	1	US-08-133-711-43	Sequence 43, Appl
c	27	14	70.0	6822	4	US-09-426-998-3	Sequence 3, Appli
c	28	14	70.0	7741	4	US-09-426-998-4	Sequence 4, Appli
	29	13	65.0	279	1	US-07-612-674-11	Sequence 11, Appl
	30	13	65.0	306	4	US-09-147-935A-12	Sequence 12, Appl
	31	13	65.0	306	4	US-09-147-935A-14	Sequence 14, Appl
	32	13	65.0	306	4	US-09-147-935A-15	Sequence 15, Appl
	33	13	65.0	306	4	US-09-147-935A-16	Sequence 16, Appl
	34	13	65.0	306	4	US-09-147-935A-18	Sequence 18, Appl
	35	13	65.0	306	4	US-09-147-935A-47	Sequence 47, Appl
c	36	13	65.0	408	4	US-09-199-637A-222	Sequence 222, App
c	37	13	65.0	663	1	US-08-506-404D-1	Sequence 1, Appli
c	38	13	65.0	663	3	US-09-035-754-1	Sequence 1, Appli
c	39	13	65.0	720	3	US-09-094-359-3	Sequence 3, Appli
c	40	13	65.0	720	3	US-09-094-359-5	Sequence 5, Appli
c	41	13	65.0	720	3	US-09-094-359-7	Sequence 7, Appli
c	42	13	65.0	720	3	US-09-094-359-9	Sequence 9, Appli
c	43	13	65.0	720	3	US-09-172-063-11	Sequence 11, Appl
c	44	13	65.0	720	3	US-09-172-063-12	Sequence 12, Appl
c	45	13	65.0	720	3	US-09-172-063-13	Sequence 13, Appl

ALIGNMENTS

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RESULT   1
US-08-750-088A-70
; Sequence 70, Application US/08750088A
; Patent No. 6329198
;  GENERAL INFORMATION:
;    APPLICANT:  DE BEENHOUWER, HANS
;    APPLICANT:  PORTAELS, FRAN OISE
;    APPLICANT:  MACHTELINCKX, LIEVE
;    APPLICANT:  JANNES, GEERT
;    APPLICANT:  ROSSAU, RUDI
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF THE ANTIBIOTIC
;    TITLE OF INVENTION:  RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  US
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/750,088A
;      FILING DATE:  21-FEB-1997
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GOLDSTEIN, JORGE A.
;      REGISTRATION NUMBER:  29,021
;      REFERENCE/DOCKET NUMBER:  1657.0010000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  70:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-750-088A-70


  Query Match           100.0%;  Score 20;  DB 4;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0.0027;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      1 TACGGTCGGCGAGCTGATCC 20


RESULT   2
US-09-147-935A-2
; Sequence 2, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 2
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium africanum
US-09-147-935A-2


  Query Match            100.0%;  Score 20;  DB 4;  Length 306;
  Best Local Similarity  100.0%;  Pred. No. 0.0022;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 tacggtcggcgagctgatcc 24


RESULT   3
US-09-147-935A-6
; Sequence 6, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 6
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium bovis
US-09-147-935A-6


  Query Match            100.0%;  Score 20;  DB 4;  Length 306;
  Best Local Similarity  100.0%;  Pred. No. 0.0022;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 tacggtcggcgagctgatcc 24


RESULT   4
US-09-147-935A-7
; Sequence 7, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 7
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium bovis BCG
US-09-147-935A-7


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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      5 tacggtcggcgagctgatcc 24


RESULT   5
US-09-147-935A-41
; Sequence 41, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 41
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-41


  Query Match            100.0%;  Score 20;  DB 4;  Length 306;
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      5 tacggtcggcgagctgatcc 24


RESULT   6
US-09-147-935A-50
; Sequence 50, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
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;       ZIP:  20005-3934
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/750,088A
;       FILING DATE:  21-FEB-1997
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  GOLDSTEIN, JORGE A.
;       REGISTRATION NUMBER:  29,021
;       REFERENCE/DOCKET NUMBER:  1657.0010000
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2540
;   INFORMATION FOR SEQ ID NO:  30:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  25 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-750-088A-30


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  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT  13
US-09-147-935A-4
; Sequence 4, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:  A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:  50
;  SOFTWARE:  KOPATIN 1.0
; SEQ ID NO 4
;  LENGTH: 306
;  TYPE: DNA
;  ORGANISM: Mycobacterium aurum
US-09-147-935A-4


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Db      9 gtcggcgagctgatcc 24


RESULT  14
US-09-147-935A-9
; Sequence 9, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:  A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:  50
;  SOFTWARE:  KOPATIN 1.0
; SEQ ID NO 9
;  LENGTH: 306
;  TYPE: DNA
;  ORGANISM: Mycobacterium celatum Type2
US-09-147-935A-9


  Query Match             80.0%;  Score 16;  DB 4;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 0.46;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      9 gtcggcgagctgatcc 24


RESULT  15
US-09-147-935A-10
; Sequence 10, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:  A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:  50
;  SOFTWARE:  KOPATIN 1.0
; SEQ ID NO 10
;  LENGTH: 306
;  TYPE: DNA
;  ORGANISM: Mycobacterium chelonae
US-09-147-935A-10


  Query Match             80.0%;  Score 16;  DB 4;  Length 306;
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  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 gtcggcgagctgatcc 20
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Db      9 gtcggcgagctgatcc 24


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Job time: 7178 sec
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OM nucleic - nucleic search, using sw model

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Title: US-09-786-105-1
Perfect score: 20
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Scoring table: [redacted]
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Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	306	1	AF057450	AF057450 Mycobacte
2	20	100.0	306	1	AF057451	AF057451 Mycobacte
3	20	100.0	306	1	AF057452	AF057452 Mycobacte
4	20	100.0	306	1	AF057453	AF057453 Mycobacte
5	20	100.0	306	1	AF057454	AF057454 Mycobacte
6	20	100.0	306	6	AR157003	AR157003 Sequence
7	20	100.0	306	6	AR157007	AR157007 Sequence
8	20	100.0	306	6	AR157008	AR157008 Sequence
9	20	100.0	306	6	AR157042	AR157042 Sequence
10	20	100.0	306	6	AR157051	AR157051 Sequence
11	20	100.0	432	1	MSGRIFRNAP	L05910 Mycobacteri
12	20	100.0	432	6	AR067448	AR067448 Sequence
13	20	100.0	970	6	I50706	I50706 Sequence 1
14	20	100.0	3534	6	AX111339	AX111339 Sequence
15	20	100.0	3853	1	MTU12205	U12205 Mycobacteri
16	20	100.0	5084	1	MSGRPOB	L27989 Mycobacteri
17	20	100.0	19352	1	AE006964	AE006964 Mycobacte
18	20	100.0	19770	1	MTCI376	Z95972 Mycobacteri
19	19	95.0	306	1	AF057493	AF057493 Mycobacte
20	19	95.0	306	6	AR157045	AR157045 Sequence
21	18	90.0	25	6	A47816	A47816 Sequence 30
C 22	18	90.0	87	6	AX050338	AX050338 Sequence
23	17	85.0	17407	1	AE006976	AE006976 Mycobacte
24	17	85.0	68848	1	MTV043	AL022004 Mycobacte
25	16	80.0	306	1	AF057456	AF057456 Mycobacte
26	16	80.0	306	1	AF057459	AF057459 Mycobacte
27	16	80.0	306	1	AF057460	AF057460 Mycobacte
28	16	80.0	306	1	AF057463	AF057463 Mycobacte
29	16	80.0	306	1	AF057471	AF057471 Mycobacte
30	16	80.0	306	1	AF057473	AF057473 Mycobacte
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32	16	80.0	306	1	AF057489	AF057489 Mycobacte
33	16	80.0	306	1	AF057496	AF057496 Corynebac
34	16	80.0	306	1	AF173087	AF173087 Mycobacte
35	16	80.0	306	6	AR157005	AR157005 Sequence
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40	16	80.0	306	6	AR157024	AR157024 Sequence
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ALIGNMENTS

RESULT 1
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LOCUS AF057450 306 bp DNA linear BCT 17-SEP-1999
DEFINITION Mycobacterium africanum RNA polymerase beta (rpoB) gene, partial cds.
ACCESSION AF057450
VERSION AF057450.1 GI:5902487
KEYWORDS .
SOURCE Mycobacterium africanum.
ORGANISM Mycobacterium africanum
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T., Kim,E.C., Cha,C.Y. and Kook,Y.H.
TITLE Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)
JOURNAL J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
MEDLINE 99262756
PUBMED 10325313
REFERENCE 2 (bases 1 to 306)
AUTHORS Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,

```
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
     source          1. .306
                     /organism="Mycobacterium africanum"
                     /strain="ATCC25420"
                     /db_xref="ATCC:25420"
                     /db_xref="taxon:33894"
     gene            <1. .>306
                     /gene="rpoB"
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                     /codon_start=3
                     /transl_table=11
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                     /db_xref="GI:5902488"
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BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
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Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   2
AF057451
LOCUS       AF057451                306 bp    DNA     linear   BCT 17-SEP-1999
DEFINITION  Mycobacterium bovis RNA polymerase beta (rpoB) gene, partial cds.
ACCESSION   AF057451
VERSION     AF057451.1  GI:5902489
KEYWORDS    .
SOURCE      Mycobacterium bovis.
  ORGANISM  Mycobacterium bovis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
  MEDLINE   99262756
   PUBMED   10325313
REFERENCE   2  (bases 1 to 306)
  AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
     source          1. .306
                     /organism="Mycobacterium bovis"
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BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 1;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
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Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   3
AF057452
LOCUS       AF057452                306 bp    DNA     linear   BCT 17-SEP-1999
DEFINITION  Mycobacterium bovis BCG strain French 1173P2 RNA polymerase beta
            (rpoB) gene, partial cds.
ACCESSION   AF057452
VERSION     AF057452.1  GI:5902491
KEYWORDS    .
SOURCE      Mycobacterium bovis BCG.
  ORGANISM  Mycobacterium bovis BCG
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
  MEDLINE   99262756
   PUBMED   10325313
REFERENCE   2  (bases 1 to 306)
  AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
     source          1. .306
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                     /strain="French 1173P2"
                     /db_xref="taxon:33892"
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                     /codon_start=3
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                     /protein_id="AAD55516.1"
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                     /translation="RTVGELIQNQIRVGMSRMERVVRERMTTQDVEAITPQTLINIRP
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BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 1;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
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Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   4
AF057453
LOCUS       AF057453                306 bp    DNA     linear   BCT 17-SEP-1999
DEFINITION  Mycobacterium bovis BCG RNA polymerase beta (rpoB) gene, partial
            cds.
ACCESSION   AF057453
VERSION     AF057453.1  GI:5902493
KEYWORDS    .
SOURCE      Mycobacterium bovis BCG.
  ORGANISM  Mycobacterium bovis BCG
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
  MEDLINE   99262756
   PUBMED   10325313
REFERENCE   2  (bases 1 to 306)
  AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
     source          1. .306
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     gene            <1. .>306
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                     /protein_id="AAD55517.1"
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BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


  Query Match           100.0%;  Score 20;  DB 1;  Length 306;
  Best Local Similarity  100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   5
AF057454
LOCUS       AF057454                306 bp    DNA     linear   BCT 08-OCT-1999
DEFINITION  Mycobacterium tuberculosis RNA polymerase beta (rpoB) gene, partial
            cds.
ACCESSION   AF057454
VERSION     AF057454.1  GI:5902495
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
  MEDLINE   99262756
   PUBMED   10325313
REFERENCE   2  (bases 1 to 306)
  AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
     source          1. .306
                     /organism="Mycobacterium tuberculosis"
                     /strain="H37Rv; ATCC27294"
                     /db_xref="ATCC:27294"
                     /db_xref="taxon:1773"
     gene            <1. .>306
                     /gene="rpoB"
     CDS             <1. .>306
                     /gene="rpoB"
                     /codon_start=3
                     /transl_table=11
                     /product="RNA polymerase beta"
                     /protein_id="AAD55518.1"
                     /db_xref="GI:5902496"
                     /translation="RTVGELIQNQIRVGMSRMERVVRERMTTQDVEAITPQTLINIRP
                     VVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDVHPSH"
BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


  Query Match           100.0%;  Score 20;  DB 1;  Length 306;
  Best Local Similarity  100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   6
AR157003
LOCUS       AR157003                306 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6242584.
ACCESSION   AR157003
VERSION     AR157003.1  GI:15125707
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kook,Y. and Kim,B.
  TITLE     Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
  JOURNAL   Patent: US 6242584-A 2 05-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .306
                     /organism="unknown"
BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


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  Best Local Similarity  100.0%;  Pred. No. 4.6;
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Qy      1 tacggtcggcgagctgatcc 20
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Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   7
AR157007
LOCUS       AR157007                306 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 6 from patent US 6242584.
ACCESSION   AR157007
VERSION     AR157007.1  GI:15125711
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kook,Y.-H. and Kim,B.-J.
  TITLE     Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
  JOURNAL   Patent: US 6242584-A 6 05-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .306
                     /organism="unknown"
BASE COUNT       56 a     96 c    107 g     47 t
ORIGIN


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Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   8
AR157008
LOCUS       AR157008                306 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 7 from patent US 6242584.
ACCESSION   AR157008
VERSION     AR157008.1  GI:15125712
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kook,Y. and Kim,B.
  TITLE     Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
  JOURNAL   Patent: US 6242584-A 7 05-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .306
                     /organism="unknown"
BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


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Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   9
AR157042
LOCUS       AR157042                306 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 41 from patent US 6242584.
ACCESSION   AR157042
VERSION     AR157042.1  GI:15125746
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kook,Y. and Kim,B.
  TITLE     Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
  JOURNAL   Patent: US 6242584-A 41 05-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .306
                     /organism="unknown"
BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


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Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT  10
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LOCUS       AR157051                306 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 50 from patent US 6242584.
ACCESSION   AR157051
VERSION     AR157051.1  GI:15125755
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kook,Y. and Kim,B.
  TITLE     Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
  JOURNAL   Patent: US 6242584-A 50 05-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .306
                     /organism="unknown"
BASE COUNT       56 a     94 c    108 g     48 t
ORIGIN


  Query Match            100.0%;  Score 20;  DB 6;  Length 306;
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT  11
MSGRIFRNAP
LOCUS       MSGRIFRNAP              432 bp    DNA     linear   BCT 21-MAY-1993
DEFINITION  Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin
            resistance gene, complete cds.
ACCESSION   L05910
VERSION     L05910.1  GI:149991
KEYWORDS    RNA polymerase beta-subunit; rifampicin resistance.
SOURCE      Mycobacterium tuberculosis (strain H37) DNA.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 432)
  AUTHORS   Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T.,
            Colston,J., Matter,L., Schopfer,K. and Bodmer,T.
  TITLE     Detection of rifampicin-resistance mutation in Mycobacterium
            tuberculosis
  JOURNAL   Antimicrob. Agents Chemother. 341, 647-650 (1993)
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FEATURES             Location/Qualifiers
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                     /organism="Mycobacterium tuberculosis"
                     /strain="H37"
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                     /db_xref="GI:149992"
                     /translation="GNRRLRTVGELIQNQIRVGMSRMERVVRERMTTQDVEAITPQTL
                     INIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDV
                     HPSHYGRMCPIETPEGPNIGLIGSLSVYARVNPFGFIETPYR"
     variation       149
                     /phenotype="rifampicin resistant in association with
                     mutation 234 G"
                     /replace="c"
     variation       188
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                     /replace="c"
     variation       191
                     /phenotype="rifampicin resistant in association with
                     mutation 203 T"
                     /replace="c"
     variation       194
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     variation       203
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BASE COUNT       77 a    140 c    148 g     67 t
ORIGIN


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  Best Local Similarity  100.0%;  Pred. No. 4.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db     18 TACGGTCGGCGAGCTGATCC 37
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RESULT  12
AR067448
LOCUS       AR067448               432 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 59 from patent US 5851763.
ACCESSION   AR067448
VERSION     AR067448.1  GI:5998670
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 432)
  AUTHORS   Heym,B., Cole,S., Young,D., Zhang,Y., Honore,N., Telenti,A. and
            Bodmer,T.
  TITLE     Rapid detection of antibiotic resistance in mycobacterium
            tuberculosis
  JOURNAL   Patent: US 5851763-A 59 22-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .432
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BASE COUNT       77 a    139 c    149 g     67 t
ORIGIN


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Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db     18 TACGGTCGGCGAGCTGATCC 37


RESULT  13
I50706
LOCUS       I50706                 970 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1 from patent US 5643723.
ACCESSION   I50706
VERSION     I50706.1  GI:2472409
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 970)
  AUTHORS   Persing,D.H., Hunt,J.J., Young,K.K.Y., Felmlee,T.A., Roberts,G.D.
            and Whelan,A.Christian.
  TITLE     Detection of a genetic locus encoding resistance to rifampin in
            mycobacterial cultures and in clinical specimens
  JOURNAL   Patent: US 5643723-A 1 01-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .970
                     /organism="unknown"
BASE COUNT      182 a    302 c    330 g    156 t
ORIGIN


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  Best Local Similarity  100.0%;  Pred. No. 3.8;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db    261 TACGGTCGGCGAGCTGATCC 280


RESULT  14
AX111339
LOCUS       AX111339               3534 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 2072 from Patent WO0123604.
ACCESSION   AX111339
VERSION     AX111339.1  GI:13927631
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
```

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  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 3534)
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 2072 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .3534
                     /organism="Mycobacterium tuberculosis"
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BASE COUNT      679 a   1081 c   1188 g    586 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 tacggtcggcgagctgatcc 20
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Db    1137 TACGGTCGGCGAGCTGATCC 1156
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RESULT 15
MTU12205
LOCUS       MTU12205                3853 bp    DNA     linear   BCT 02-MAR-2000
DEFINITION  Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
            gene, partial cds.
ACCESSION   U12205
VERSION     U12205.1  GI:515684
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 3853)
  AUTHORS   Imboden,P., Troller,R., Marchesi,F., Telenti,A., Bodmer,T.,
            Cole,S., Schopfer,K. and Burkart,T.
  TITLE     The rpoB gene of Mycobacterium tuberculosis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3853)
  AUTHORS   Imboden,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-1994) Paul Imboden, Institute for Medical
            Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
            3010, Switzerland
FEATURES             Location/Qualifiers
     source          1. .3853
                     /organism="Mycobacterium tuberculosis"
                     /strain="H37Rv"
                     /db_xref="taxon:1773"
     gene            576. .>3853
                     /gene="rpoB"
     CDS             576. .>3853
                     /gene="rpoB"
                     /codon_start=1
                     /transl_table=11
                     /product="RNA-polymerase beta subunit"
                     /protein_id="AAA20242.2"
                     /db_xref="GI:7144499"
                     /translation="MLEGCILADSRQSKTAASPSPSRPQSSSNNSVPGAPNRVSFAKL
                     REPLEVPGLLDVQTDSFEWLIGSPRWRESAAERGDVNPVGGLEEVLYELSPIEDFSGS
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                     TEKGTFIINGTERVVVSQLVRSPGVYFDETIDKSTDKTLHSVKVIPSRGAWLEFDVDK
                     RDTVGVRIDRKRRQPVTVLLKALGWTSEQIVERFGFSEIMRSTLEKDNTVGTDEALLD
                     IYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARVGRYKVNKKLGLHVGEPITSSTLT
                     EEDVVATIEYLVRLHEGQTTMTVPGGVEVPVETDDIDHFGNRRLRTVGELIQNQIRVG
                     MSRMERVVRERMTTQDVEAITPQTLINIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLT
                     HKRRLSALGPGGLSRERAGLEVRDVHPSHYGRMCPIETPEGPNIGLIGSLSVYARVNP
                     FGFIETPYRKVVDGVVSDGIVYLTADEEDRHVVAQANSPIDADGRFVEPRVLVRRKAG
                     EVEYVPSSEVDYMDVSPRQMVSVATAMIPFLEHDDANRALMGANMQRQAVPLVRSEAP
                     LVGTGMELRAAIDAATSSSQESGVIEEVSADYITVMHDNGTRRTYRMRKFARSNHGTC
                     ANQCPIVDAGDRVEAGQVIADGPCTDDGEMALGKNLLVAIMPWEGHNYEDAIILSNRL
                     VEEDVLTSIHIEEHEIDARDTKLGAEEITRDIPNISDEVLADLDERGIVRIGAEVRDG
                     DILVGKVTPKGETELTPEERLLRAIFGEKAREVRDTSLKVPHGESGKVIGIRVFSRED
                     EDELPAGVNELVRVYVAQKRKISDGDKLAGRHGNKGVIGKILPVEDMPFLADGTPVDI
                     ILNTHGVPRRMNIGQILETHLGWCAHSGWKVDAAKGVPDWAARLPDELLEAQPNAIVS
                     TPVFDGAQEAELQGLLSCTLPNRDGDVLVDADGKAMLFDGRSGEPFPYPVTVGYMYIM
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BASE COUNT      723 a   1173 c   1293 g    664 t
ORIGIN
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Query Match 100.0%; Score 20; DB 1; Length 3853;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 tacggtcggcgagctgatcc 20
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Db    1712 TACGGTCGGCGAGCTGATCC 1731
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GenCore version 4.5

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Gapop 60.0 , Gapext 60.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	17	85.0	422	10	BE443802	BE443802 WHE1122_B
2	17	85.0	544	10	BE445100	BE445100 WHE1132_H
3	17	85.0	558	10	BE444713	BE444713 WHE1137_H
4	17	85.0	610	9	BE195103	BE195103 HVSMEh008
5	17	85.0	658	10	BE442518	BE442518 WHE1101_H
6	17	85.0	828	10	BG299722	BG299722 HVSMEa002
c 7	16	80.0	130	10	BM397871	BM397871 5009-0-38
c 8	16	80.0	132	10	BM396091	BM396091 5009-0-17
c 9	16	80.0	134	10	BM398255	BM398255 5009-0-42
c 10	16	80.0	606	10	BI981973	BI981973 fu53f08.y
c 11	16	80.0	640	10	BI888442	BI888442 ZF637-2-0
12	16	80.0	708	10	BE585978	BE585978 Est#7pT7_
c 13	15	75.0	237	10	BE423869	BE423869 WHE0067_F
14	15	75.0	376	9	AI945868	AI945868 bs17g07.y
15	15	75.0	379	9	AI944952	AI944952 bs07c12.y
c 16	15	75.0	556	12	BH229591	BH229591 1006153C0
17	15	75.0	568	10	BI628597	BI628597 RH57079.5
18	15	75.0	652	10	BF489438	BF489438 AT25558.5
19	15	75.0	655	10	BF489430	BF489430 AT25548.5
20	15	75.0	667	10	BF489536	BF489536 AT25583.5
21	15	75.0	703	10	BF496035	BF496035 AT09742.5
22	15	75.0	722	10	BF496005	BF496005 AT09708.5
23	15	75.0	958	10	BE969326	BE969326 601649529
c 24	15	75.0	984	12	CNS01GJZ	AL143232 Anopheles
c 25	15	75.0	1000	10	BG416363	BG416363 HVSMEk001
c 26	15	75.0	1188	10	BM477266	BM477266 AGENCOURT
27	14	70.0	159	10	BI727507	BI727507 1031093A0
28	14	70.0	180	10	C61884	C61884 C61884 Yuji
29	14	70.0	239	10	BF920601	BF920601 QV0-NT015
30	14	70.0	251	12	AQ906217	AQ906217 GSSTc0226
c 31	14	70.0	252	10	W87730	W87730 zh65g09.s1
c 32	14	70.0	292	9	BB347857	BB347857 BB347857
33	14	70.0	299	10	BI133481	BI133481 UI-M-BH3-
c 34	14	70.0	318	10	M79472	M79472 wEST00009 M
35	14	70.0	328	9	AW922029	AW922029 EST353333
c 36	14	70.0	329	10	H57342	H57342 yr11c05.s1
37	14	70.0	339	9	AJ281216	AJ281216 4A3A-ABC-
38	14	70.0	344	10	BE415176	BE415176 MWL024.B0
c 39	14	70.0	349	9	AU110574	AU110574 AU110574
c 40	14	70.0	349	10	BG274757	BG274757 WHE2233_G
41	14	70.0	352	10	T83696	T83696 yd65c08.r1
c 42	14	70.0	360	9	AV186178	AV186178 AV186178
c 43	14	70.0	360	9	AV191317	AV191317 AV191317
c 44	14	70.0	360	9	AV192208	AV192208 AV192208
c 45	14	70.0	360	9	AV197881	AV197881 AV197881

ALIGNMENTS

RESULT 1
BE443802
LOCUS BE443802 422 bp mRNA linear EST 25-JUL-2000
DEFINITION WHE1122_B06_C12ZS Wheat etiolated seedling root normalized cDNA library Triticum aestivum cDNA clone WHE1122_B06_C12, mRNA sequence.
ACCESSION BE443802
VERSION BE443802.1 GI:9443341
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 422)
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
TITLE The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
FEATURES Location/Qualifiers
source 1. .422
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1122_B06_C12"
/clone_lib="Wheat etiolated seedling root normalized cDNA library"
/tissue_type="Root"

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                     /dev_stage="Five day old etiolated seedling"
                     /lab_host="E. coli DH10B"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid
                     pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
                     surface-sterilized, germinated and grown aseptically in
                     the  dark at room temperature on filter paper with water,
                     nystatin and  cefotaxime in covered crystallization
                     dishes. Roots were harvested.  The tissue, total RNA, and
                     poly(A) RNA were prepared, a cDNA library  was made in the
                     TJ Close lab (Choi, Close, Fenton) at the University  of
                     California, Riverside.  The cDNA clones were in vivo
                     excised to  give pBluescript phagemids before
                     normalization was carried out.   The mass excision of
                     phagemid library and normalization were done in HT  Nguyen
                     lab by D. Zhang at Texas Tech Univeristy.  Normalization
                     protocol used was that of Soares.  Plasmid DNA
                     preparations and DNA  sequencing were performed in the OD
                     Anderson lab (all other authors)."
BASE COUNT       84 a    130 c    124 g     84 t
ORIGIN


  Query Match             85.0%;  Score 17;  DB 10;  Length 422;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 ggtcggcgagctgatcc 20
           |||||||||||||||||
Db      86 GGTCGGCGAGCTGATCC 102


RESULT   2
BE445100
LOCUS       BE445100                 544 bp    mRNA    linear   EST 25-JUL-2000
DEFINITION  WHE1132_H08_P16ZS Wheat etiolated seedling root normalized cDNA
            library Triticum aestivum cDNA clone WHE1132_H08_P16, mRNA
            sequence.
ACCESSION   BE445100
VERSION     BE445100.1  GI:9444655
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 544)
  AUTHORS   Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
            ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
            Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Normalized root cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES             Location/Qualifiers
     source          1. .544
                     /organism="Triticum aestivum"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="WHE1132_H08_P16"
                     /clone_lib="Wheat etiolated seedling root normalized cDNA
                     library"
                     /tissue_type="Root"
                     /dev_stage="Five day old etiolated seedling"
                     /lab_host="E. coli DH10B"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid
                     pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
                     surface-sterilized, germinated and grown aseptically in
                     the  dark at room temperature on filter paper with water,
                     nystatin and  cefotaxime in covered crystallization
                     dishes. Roots were harvested.  The tissue, total RNA, and
                     poly(A) RNA were prepared, a cDNA library  was made in the
                     TJ Close lab (Choi, Close, Fenton) at the University  of
                     California, Riverside.  The cDNA clones were in vivo
                     excised to  give pBluescript phagemids before
                     normalization was carried out.   The mass excision of
                     phagemid library and normalization were done in HT  Nguyen
                     lab by D. Zhang at Texas Tech Univeristy.  Normalization
                     protocol used was that of Soares.  Plasmid DNA
                     preparations and DNA  sequencing were performed in the OD
                     Anderson lab (all other authors)."
BASE COUNT      121 a    173 c    132 g    118 t
ORIGIN


  Query Match             85.0%;  Score 17;  DB 10;  Length 544;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 ggtcggcgagctgatcc 20
           |||||||||||||||||
Db     512 GGTCGGCGAGCTGATCC 528


RESULT   3
BE444713
LOCUS       BE444713                 558 bp    mRNA    linear   EST 25-JUL-2000
DEFINITION  WHE1137_H03_O05ZS Wheat etiolated seedling root normalized cDNA
            library Triticum aestivum cDNA clone WHE1137_H03_O05, mRNA
            sequence.
ACCESSION   BE444713
VERSION     BE444713.1  GI:9444264
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 558)
  AUTHORS   Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
            ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
            Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Normalized root cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES             Location/Qualifiers
     source          1. .558
                     /organism="Triticum aestivum"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="WHE1137_H03_O05"
                     /clone_lib="Wheat etiolated seedling root normalized cDNA
                     library"
                     /tissue_type="Root"
                     /dev_stage="Five day old etiolated seedling"
                     /lab_host="E. coli DH10B"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid
                     pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
```

surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. The cDNA clones were in vivo excised to give pBluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech Univeristy. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 122 a 180 c 134 g 122 t
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 558;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ggtcggcgagctgatcc 20
||||||||||||||||
Db 514 GGTCGGCGAGCTGATCC 530

RESULT 4
BE195103
LOCUS BE195103 610 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEh0088E21f Hordeum vulgare 5-45 DAP spike EST library HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0088E21f, mRNA sequence.
ACCESSION BE195103
VERSION BE195103.3 GI:16321083
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 610)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton ,R.D., Close,S.J., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex 5-45 DAP spike cDNA library
JOURNAL Unpublished (2001)
COMMENT On Jun 26, 2000 this sequence version replaced gi:13187931.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 238
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 563.
FEATURES Location/Qualifiers
source 1. .610
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEh0088E21f"
/clone_lib="Hordeum vulgare 5-45 DAP spike EST library HVcDNA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Plants were grown in the greenhouse at the University of California, Riverside (Fenton, SJ Close, TJ Close). Whole spikes with awns trimmed were collected at 5, 10, 15, 20, 30 and 45 DAP (Fenton). Total RNA was prepared from each pool, equal quantities of all six RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi)in the TJ Close lab at the University of California, Riverside. Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 127 a 203 c 158 g 120 t 2 others
ORIGIN

Query Match 85.0%; Score 17; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ggtcggcgagctgatcc 20
||||||||||||||||
Db 499 GGTCGGCGAGCTGATCC 515

RESULT 5
BE442518
LOCUS BE442518 658 bp mRNA linear EST 25-JUL-2000
DEFINITION WHE1101_H10_019ZS Wheat etiolated seedling root normalized cDNA library Triticum aestivum cDNA clone WHE1101_H10_019, mRNA sequence.
ACCESSION BE442518
VERSION BE442518.1 GI:9442034
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 658)
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
TITLE The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
FEATURES Location/Qualifiers
source 1. .658
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1101_H10_019"
/clone_lib="Wheat etiolated seedling root normalized cDNA library"

/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. The cDNA clones were in vivo excised to give pBluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech Univeristy. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
BASE COUNT 144 a 209 c 165 g 140 t
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 658;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ggtcggcgagctgatcc 20
||||||||||||||||
Db 512 GGTCGGCGAGCTGATCC 528

RESULT 6
BG299722
LOCUS BG299722 828 bp mRNA linear EST 17-OCT-2001
DEFINITION HVSMEa0021I20f Hordeum vulgare seedling shoot EST library HVcDNA0001 (Cold stress) Hordeum vulgare cDNA clone HVSMEa0021I20f, mRNA sequence.
ACCESSION BG299722
VERSION BG299722.1 GI:13087434
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 828)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R., Choi,D.W., Fenton,R.D. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex cold-stressed seedling shoot cDNA library
JOURNAL Unpublished (2001)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 574
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 643.
FEATURES Location/Qualifiers
source 1. .828
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEa0021I20f"
/clone_lib="Hordeum vulgare seedling shoot EST library HVcDNA0001 (Cold stress)"
/tissue_type="Seedling shoot"
/lab_host="TJC121"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedlings were incubated at 5oC for 2 days. Shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 600000 pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT 172 a 271 c 220 g 165 t
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 828;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ggtcggcgagctgatcc 20
||||||||||||||||
Db 500 GGTCGGCGAGCTGATCC 516

RESULT 7
BM397871/c
LOCUS BM397871 130 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-38-C10.t.1 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM397871
VERSION BM397871.1 GI:18197924
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 130)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .130
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001)

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                    Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT       26 a     41 c     44 g     18 t      1 others
ORIGIN

  Query Match             80.0%;  Score 16;  DB 10;  Length 130;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 gtcggcgagctgatcc 20
          ||||||||||||||||
Db     90 GTCGGCGAGCTGATCC 75


RESULT   8
BM396091/c
LOCUS       BM396091                 132 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-17-B01.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM396091
VERSION     BM396091.1  GI:18196144
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila.
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1  (bases 1 to 132)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
            ,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .132
                     /organism="Tetrahymena thermophila"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT       27 a     42 c     44 g     19 t
ORIGIN

  Query Match             80.0%;  Score 16;  DB 10;  Length 132;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 gtcggcgagctgatcc 20
          ||||||||||||||||
Db     92 GTCGGCGAGCTGATCC 77


RESULT   9
BM398255/c
LOCUS       BM398255                 134 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-42-H08.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM398255
VERSION     BM398255.1  GI:18198308
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila.
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1  (bases 1 to 134)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
            ,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .134
                     /organism="Tetrahymena thermophila"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT       26 a     44 c     46 g     18 t
ORIGIN

  Query Match             80.0%;  Score 16;  DB 10;  Length 134;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 gtcggcgagctgatcc 20
          ||||||||||||||||
Db     94 GTCGGCGAGCTGATCC 79


RESULT  10
BI981973/c
LOCUS       BI981973                 606 bp    mRNA    linear   EST 24-OCT-2001
DEFINITION  fu53f08.y1 zebrafish adult brain Danio rerio cDNA clone 5333151 5'
            similar to TR:Q9Y4D4 Q9Y4D4 KIAA0648 PROTEIN ;, mRNA sequence.
ACCESSION   BI981973
VERSION     BI981973.1  GI:16371108
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 606)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
            ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
            ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
            Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
            Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
            and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Other_ESTs: fu53f08.x1
            Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
            Matthew Clark. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
            www.rzpd.de)
            High quality sequence stop: 446.
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FEATURES             Location/Qualifiers
     source          1. .606
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone="5333151"
                     /clone_lib="zebrafish adult brain"
                     /sex="mixed male and female"
                     /tissue_type="brain"
                     /dev_stage="adult"
                     /lab_host="E. coli DH10B"
                     /note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
                     Original library was constructed in lambdaZIPLOX.  Mass
                     excision of the cDNA library was performed to yield
                     pZIPLOX plasmids. Insert check was done in original
                     library."
BASE COUNT      209 a    133 c    139 g    125 t
ORIGIN


  Query Match             80.0%;  Score 16;  DB 10;  Length 606;
  Best Local Similarity   100.0%;  Pred. No. 74;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctg 16
          ||||||||||||||||
Db    452 TACGGTCGGCGAGCTG 437


RESULT  11
BI888442/c
LOCUS       BI888442                640 bp    mRNA    linear   EST 12-OCT-2001
DEFINITION  ZF637-2-000197 Zebrafish shield stage whole embryo cDNA library
            MPMGp637 Danio rerio cDNA clone MPMGp637_18E17;MPMGp637E1718 5',
            mRNA sequence.
ACCESSION   BI888442
VERSION     BI888442.1  GI:16095713
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 640)
  AUTHORS   Clark,M., Aanstad,P., Hennig,S., Johnson,S.L. and Lehrach,H.
  TITLE     EST sequencing of a zebrafish shield stage cDNA library normalised
            by oligonucleotide fingerprinting
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Hennig S
            laboraty 123, dept.Lehrach
            Max-Planck-Institut fuer Molekulare Genetik
            Ihnestr.63-73, D-14195 Berlin, Germany
            Tel: +49 30 8413 1612
            Fax: +49 30 8413 1380
            Email: hennig@molgen.mpg.de
            5' EST sequencing of clones from a zebrafish shield stage library,
            normalised from 55,000 starting clones by oligonucleotide
            fingerprinting
            High quality sequence stop: 640.
FEATURES             Location/Qualifiers
     source          1. .640
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone="MPMGp637_18E17;MPMGp637E1718"
                     /clone_lib="Zebrafish shield stage whole embryo cDNA
                     library MPMGp637"
                     /tissue_type="whole embryo"
                     /dev_stage="shield stage, 6 hrs post-fertilisation"
                     /lab_host="E.coli, XL1 blue MRF"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI;
                     oligo-dT-NotI primed, SalI adaptors, directionally cloned,
                     library normalised by oligonucleotide fingerprinting"
BASE COUNT      209 a    152 c    139 g    139 t      1 others
ORIGIN


  Query Match             80.0%;  Score 16;  DB 10;  Length 640;
  Best Local Similarity   100.0%;  Pred. No. 74;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctg 16
          ||||||||||||||||
Db    541 TACGGTCGGCGAGCTG 526


RESULT  12
BE585978
LOCUS       BE585978                708 bp    mRNA    linear   EST 17-AUG-2000
DEFINITION  Est#7pT7_A09_a9_065 KSU wheat Fusarium graminearum infected spike
            cDNA library Triticum aestivum cDNA clone Est#7pT7_A09_a9_065, mRNA
            sequence.
ACCESSION   BE585978
VERSION     BE585978.1  GI:9839010
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 708)
  AUTHORS   Fellers,J.P., Li,W.L., Hill-Ambroz,K., Matthews,A. and Gill,B.S.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Kansas State Unversity. Fusarium graminearum infected
            spike cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: John Fellers
            US Department of Agriculture, Agriculture Research Service, Plant
            Science and Entomology Unit
            Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State
            University, Manhattan, KS 66506, USA
            Tel: 785-532-2367
            Fax: 785-532-6167
            Email: jpf@alfalfa.ksu.edu
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .708
                     /organism="Triticum aestivum"
                     /cultivar="Sumai3"
                     /db_xref="taxon:4565"
                     /clone="Est#7pT7_A09_a9_065"
                     /clone_lib="KSU wheat Fusarium graminearum infected spike
                     cDNA library"
                     /tissue_type="Spike"
                     /dev_stage="Adult plant"
                     /lab_host="E. coli JM109"
                     /note="Vector: pGEM-T easy; Site_1: SacII; Site_2: SpeI;
                     Plants were grown in the greenhouse. Spikes were sprayed
                     with  Fusarium graminearum (at what stage). Total RNA, and
                     poly(A) RNA  were prepared from infected spikes. cDNA was
                     prepared using the  SmartTM PCR cDNA synthesis kit from
                     Clonetech. cDNA was cloned  into the pGEM-T easy vector
                     from Promega."
BASE COUNT      154 a    221 c    177 g    156 t
ORIGIN


  Query Match             80.0%;  Score 16;  DB 10;  Length 708;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 gtcggcgagctgatcc 20
          ||||||||||||||||
Db    559 GTCGGCGAGCTGATCC 574
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RESULT 13
BE423869/c
LOCUS       BE423869                237 bp    mRNA    linear   EST 24-JUL-2000
DEFINITION  WHE0067_F05_K09ZS Wheat endosperm cDNA library Triticum aestivum
            cDNA clone WHE0067_F05_K09, mRNA sequence.
ACCESSION   BE423869
VERSION     BE423869.1  GI:9421712
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 237)
  AUTHORS   Altenbach,S., Anderson,O.D., Chao,S., Galili,G., Han,P.S., Hsia
            ,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and
            Tong,J.C.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Endosperm cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES             Location/Qualifiers
     source          1. .237
                     /organism="Triticum aestivum"
                     /cultivar="Cheyenne"
                     /db_xref="taxon:4565"
                     /clone="WHE0067_F05_K09"
                     /clone_lib="Wheat endosperm cDNA library"
                     /tissue_type="Endosperm"
                     /dev_stage="5 to 30 days post anthesis seed"
                     /lab_host="E. coli SOLR"
                     /note="Vector: Lambda ZAP II, excised phagemid; Site_1:
                     EcoRI; Seeds collected, endosperm isolated, and RNA
                     prepared by Susan  Altenbach. Library constructed by
                     Stratagene, Inc. Plasmid DNA  preparations and DNA
                     sequencing were performed in the OD Anderson lab."
BASE COUNT       65 a     79 c     40 g     53 t
ORIGIN


  Query Match            75.0%;  Score 15;  DB 10;  Length 237;
  Best Local Similarity  100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 tcggcgagctgatcc 20
          |||||||||||||||
Db     79 TCGGCGAGCTGATCC 65


RESULT 14
AI945868
LOCUS       AI945868                376 bp    mRNA    linear   EST 08-JAN-2001
DEFINITION  bs17g07.y1 Drosophila melanogaster adult testis library Drosophila
            melanogaster cDNA clone bs17g07 5', mRNA sequence.
ACCESSION   AI945868
VERSION     AI945868.2  GI:9991196
KEYWORDS    EST.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 376)
  AUTHORS   Andrews,J., Bouffard,G.G., Cheadle,C., Lu,J., Becker,K.G. and
            Oliver,B.
  TITLE     Gene discovery using computational and microarray analysis of
            transcription in the drosophila melanogaster testis
  JOURNAL   Genome Res. 10 (12), 2030-2043 (2000)
  MEDLINE   20568492
COMMENT     On Aug 17, 1999 this sequence version replaced gi:5736266.
            Contact: Brian Oliver
            Laboratory of Cellular and Developmental Biology
            NIDDK, National Institutes of Health
            6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethesda, MD 20892 USA
            Fax: (301) 496 5239
            Email: oliver@helix.nih.gov,
            http://www.niddk.nih.gov/intram/people/boliver.htm
            Tissue isolation and library construction performed at the National
            Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
            http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
            and analyses performed by National Institutes of Health Intramural
            Sequencing Center (NISC; see http://www.nisc.nih.gov).
            Plate: 17  row: g  column: 07
            Seq primer: M13RP1 reverse primer (ABI).
FEATURES             Location/Qualifiers
     source          1. .376
                     /organism="Drosophila melanogaster"
                     /strain="y[*] w[67c1]/Y"
                     /db_xref="taxon:7227"
                     /clone="bs17g07"
                     /clone_lib="Drosophila melanogaster adult testis library"
                     /sex="male"
                     /dev_stage="1-5 day adult"
                     /lab_host="SOLR (Stratagene)"
                     /note="Organ: testis; Vector: pBlueScript SK (Stratagene);
                     Site_1: EcoR I; Site_2: Xho I; Testes dissected from 1-5
                     day adult y[*] w[67c1]/Y males raised at 25oC.  RNA
                     isolated using Trizol (Life Technologies) and a single
                     round of Poly(A)+ selection using Oligotex (Qiagen).  cDNA
                     library constructed using Stratagene ZAP-cDNA syntesis
                     kit.  Oligo dT-primed, size fractionated ~1-6 kb, and
                     directionally cloned at EcoRI and XhoI in Uni-ZAP XR.
                     Following a single round of amplification pBlueScript SK
                     phagemids were mass excised.  A distribution channel for
                     clones is being sought, but not currently available.
                     Requests for clones cannot be honored."
BASE COUNT      110 a     94 c    107 g     65 t
ORIGIN


  Query Match            75.0%;  Score 15;  DB 9;  Length 376;
  Best Local Similarity  100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 acggtcggcgagctg 16
          |||||||||||||||
Db    272 ACGGTCGGCGAGCTG 286


RESULT 15
AI944952
LOCUS       AI944952                379 bp    mRNA    linear   EST 08-JAN-2001
DEFINITION  bs07c12.y1 Drosophila melanogaster adult testis library Drosophila
            melanogaster cDNA clone bs07c12 5', mRNA sequence.
ACCESSION   AI944952
VERSION     AI944952.2  GI:9990300
KEYWORDS    EST.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 379)
  AUTHORS   Andrews,J., Bouffard,G.G., Cheadle,C., Lu,J., Becker,K.G. and
            Oliver,B.
  TITLE     Gene discovery using computational and microarray analysis of
            transcription in the drosophila melanogaster testis
```

```
  JOURNAL   Genome Res. 10 (12), 2030-2043 (2000)
  MEDLINE   20568492
COMMENT     On Aug 17, 1999 this sequence version replaced gi:5735350.
            Contact: Brian Oliver
            Laboratory of Cellular and Developmental Biology
            NIDDK, National Institutes of Health
            6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethesda, MD 20892 USA
            Fax: (301) 496 5239
            Email: oliver@helix.nih.gov,
            http://www.niddk.nih.gov/intram/people/boliver.htm
            Tissue isolation and library construction performed at the National
            Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
            http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
            and analyses performed by National Institutes of Health Intramural
            Sequencing Center (NISC; see http://www.nisc.nih.gov).
            Plate: 07  row: c  column: 12
            Seq primer: M13RP1 reverse primer (ABI).
FEATURES             Location/Qualifiers
     source          1. .379
                     /organism="Drosophila melanogaster"
                     /strain="y[*] w[67c1]/Y"
                     /db_xref="taxon:7227"
                     /clone="bs07c12"
                     /clone_lib="Drosophila melanogaster adult testis library"
                     /sex="male"
                     /dev_stage="1-5 day adult"
                     /lab_host="SOLR (Stratagene)"
                     /note="Organ: testis; Vector: pBlueScript SK (Stratagene);
                     Site_1: EcoR I; Site_2: Xho I; Testes dissected from 1-5
                     day adult y[*] w[67c1]/Y males raised at 25oC.  RNA
                     isolated using Trizol (Life Technologies) and a single
                     round of Poly(A)+ selection using Oligotex (Qiagen).  cDNA
                     library constructed using Stratagene ZAP-cDNA syntesis
                     kit.  Oligo dT-primed, size fractionated ~1-6 kb, and
                     directionally cloned at EcoRI and XhoI in Uni-ZAP XR.
                     Following a single round of amplification pBlueScript SK
                     phagemids were mass excised.  A distribution channel for
                     clones is being sought, but not currently available.
                     Requests for clones cannot be honored."
BASE COUNT      104 a     96 c    113 g     66 t
ORIGIN


  Query Match           75.0%;  Score 15;  DB 9;  Length 379;
  Best Local Similarity  100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 acggtcggcgagctg 16
           ||||||||||||||| 
Db      39 ACGGTCGGCGAGCTG 53


Search completed: August  7, 2002, 23:12:30
Job time: 11069 sec
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:12:30 ; Search time 4095.84 Seconds
(without alignments)
65.906 Million cell updates/sec

Title: US-09-786-105-2
Perfect score: 20
Sequence: 1 tacggcgtttcgatgaaccc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	17	85.0	234	10	W06754	W06754 SMEST0390 S
c 2	17	85.0	579	10	T24127	T24127 SMEST0325 S
3	16	80.0	624	10	BE896357	BE896357 601439015
4	15	75.0	384	10	BM077908	BM077908 pb21g06.y
c 5	15	75.0	452	9	AW694629	AW694629 NF078E03S
6	15	75.0	517	12	TA247H04P	AL483262 T. brucei
7	15	75.0	536	12	AQ783856	AQ783856 HS_2001_A
8	15	75.0	537	12	TA140G03P	AL466454 T. brucei
c 9	15	75.0	540	12	TA190A10P	AL477985 T. brucei
10	15	75.0	631	12	BH615799	BH615799 BMBAC304F
11	15	75.0	690	9	BE053145	BE053145 GA__Ea000
c 12	15	75.0	1033	12	CNS040YP	AL269530 Tetraodon
13	15	75.0	1218	10	BM007170	BM007170 603614933
c 14	14	70.0	247	9	AV640031	AV640031 AV640031
c 15	14	70.0	269	9	AV640876	AV640876 AV640876
c 16	14	70.0	288	9	BB177553	BB177553 BB177553
17	14	70.0	336	12	AQ660540	AQ660540 Sheared D
c 18	14	70.0	390	9	AV644609	AV644609 AV644609
19	14	70.0	416	9	AJ284239	AJ284239 4A3B-AAU-
20	14	70.0	421	12	AZ813806	AZ813806 2M0081E16
21	14	70.0	428	10	BM252718	BM252718 SnEST4a42
22	14	70.0	431	9	AW280184	AW280184 fj52a10.x
23	14	70.0	466	9	AF051116	AF051116 AF051116
c 24	14	70.0	472	10	BE449520	BE449520 EST356279
c 25	14	70.0	474	9	AV396989	AV396989 AV396989
c 26	14	70.0	476	9	AI483656	AI483656 EST249527
c 27	14	70.0	477	9	AI488127	AI488127 EST246449
28	14	70.0	489	9	AW618736	AW618736 EST320722
c 29	14	70.0	497	9	AV643117	AV643117 AV643117
c 30	14	70.0	508	9	AV642711	AV642711 AV642711
c 31	14	70.0	518	9	AV642141	AV642141 AV642141
c 32	14	70.0	525	9	AW650840	AW650840 EST329294
c 33	14	70.0	531	9	AV642766	AV642766 AV642766
34	14	70.0	544	12	AQ843909	AQ843909 LMAJFV1_1
c 35	14	70.0	556	9	AW155814	AW155814 614097B10
c 36	14	70.0	562	12	BH487728	BH487728 BOGQP76TR
c 37	14	70.0	566	9	AV631818	AV631818 AV631818
c 38	14	70.0	582	12	CNS01K68	AL147937 Anopheles
39	14	70.0	626	9	AW442770	AW442770 EST307700
c 40	14	70.0	626	9	BB640393	BB640393 BB640393
41	14	70.0	628	10	BF270176	BF270176 GA__Eb000
42	14	70.0	664	10	BG102752	BG102752 RHIZ2_36_
43	14	70.0	670	12	AQ943645	AQ943645 Sheared D
c 44	14	70.0	672	12	AQ943372	AQ943372 Sheared D
c 45	14	70.0	676	9	AI491107	AI491107 EST241816

ALIGNMENTS

RESULT 1
W06754/c
LOCUS W06754 234 bp mRNA linear EST 01-JUL-1996
DEFINITION SMEST0390 Schistosoma mansoni, adult worm, Gloria Franco
Schistosoma mansoni cDNA clone SMPBE73 3' end, mRNA sequence.
ACCESSION W06754
VERSION W06754.1 GI:1444974
KEYWORDS EST.
SOURCE Schistosoma mansoni.
ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE 1 (bases 1 to 234)
AUTHORS Franco,G.R. and Pena,S.D.J.
TITLE Franco,G.R. and Pena,S.D.J., Unpublished
JOURNAL Unpublished (1996)
COMMENT Contact: Franco G.R. and Pena S.D.J.
Laboratorio de Genetica-Bioquimica, Departamento de Bioquimicae Imunologia
Instituto de Ciencias Biologicas, Universidade Federal de Minas Gerais
Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
Tel: (5531)4415611
Fax: (5531)4415409
Email: gfranco@mono.icb.ufmg.br
Seq primer: M13 Forward.
FEATURES Location/Qualifiers
source 1. .234
/organism="Schistosoma mansoni"
/strain="NMRI"
/db_xref="taxon:6183"
/clone="SMPBE73"
/clone_lib="Schistosoma mansoni, adult worm, Gloria Franco"
/lab_host="DH10B, JM109"
/note="Vector: BA vector; Site_1: NotI; Site_2: HindIII; Total cellular RNA from male and female adult worms was extracted according to a modification (Puissant, C. and Houdebine, L. M. BioFeedback 8, 148-149, 1990) of the Guanidine Thiocyanate procedure (Chomczynski, P. and

Sacchi, N. Anal. Biochem. 162, 156- 159, 1987). Poly (A)+ RNA was purified by oligo dT column and cDNA was synthesized as described previously (Adams, M. D. et al. Nature Genet. 4, 373-389, 1993). cDNA was ligated to a two fold molar excess of a NotI/HindIII digested plasmid DNA (lafmid BA vector, a phagemid derived from pEMBL, Adams, M. D. et al. Nature Genet. 4, 373-389, 1993)) and electroporated into E. coli strain DH10B (BRL). The library was amplified and further selected for clones containing long inserts (>500 bp) by purification of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel, containing the smear of the library and electroporation into DH10B cells. "

BASE COUNT 49 a 84 c 66 g 33 t 2 others
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 234;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaa 17
||||||||||||||||||
Db 64 TACGGCGTTTCGATGAA 48

RESULT 2
T24127/c
LOCUS T24127 579 bp mRNA linear EST 27-FEB-1995
DEFINITION SMEST0325 Schistosoma mansoni, adult worm, Gloria Franco Schistosoma mansoni cDNA clone SMPBC65 3', mRNA sequence.
ACCESSION T24127
VERSION T24127.1 GI:529730
KEYWORDS EST.
SOURCE Schistosoma mansoni.
ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE 1 (bases 1 to 579)
AUTHORS Franco,G.R., Adams,M.D., Soares,M.B., Simpson,A.J.G., Venter,J.C. and Pena,S.D.J.
TITLE Identification of new Schistosoma mansoni genes by the EST strategy using a directional cDNA library
JOURNAL Gene 152, 141-147 (1995)
MEDLINE 95137379
COMMENT Contact: Franco G.R. and Pena S.D.J.
Laboratorio de Genetica-Bioquimica, Departamento de Bioquimicae Imunologia
Instituto de Ciencias Biologicas, Universidade Federal de Minas Gerais
Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
Tel: (5531)4415611
Fax: (5531)4415409
Email: gfranco@mono.icb.ufmg.br
Seq primer: M13 Forward.
FEATURES Location/Qualifiers
source 1. .579
/organism="Schistosoma mansoni"
/strain="NMRI"
/db_xref="taxon:6183"
/clone="SMPBC65"
/clone_lib="Schistosoma mansoni, adult worm, Gloria Franco"
/lab_host="DH10B, JM109"
/note="Vector: BA vector; Site_1: NotI; Site_2: HindIII; Total cellular RNA from male and female adult worms was extracted according to a modification (Puissant, C. and Houdebine, L. M. BioFeedback 8, 148-149, 1990) of the Guanidine Thiocyanate procedure (Chomczynski, P. and Sacchi, N. Anal. Biochem. 162, 156- 159, 1987). Poly (A)+ RNA was purified by oligo dT column and cDNA was synthesized as described previously (Adams, M. D. et al. Nature Genet. 4, 373-389, 1993). cDNA was ligated to a two fold molar excess of a NotI/HindIII digested plasmid DNA (lafmid BA vector, a phagemid derived from pEMBL, Adams, M. D. et al. Nature Genet. 4, 373-389, 1993)) and electroporated into E. coli strain DH10B (BRL). The library was amplified and further selected for clones containing long inserts (>500 bp) by purification of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel, containing the smear of the library and electroporation into DH10B cells. "

BASE COUNT 102 a 206 c 179 g 88 t 4 others
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaa 17
||||||||||||||||||
Db 75 TACGGCGTTTCGATGAA 59

RESULT 3
BE896357
LOCUS BE896357 624 bp mRNA linear EST 20-OCT-2000
DEFINITION 601439015F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924266 5', mRNA sequence.
ACCESSION BE896357
VERSION BE896357.1 GI:10360678
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 624)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9761 row: m column: 03
High quality sequence start: 2
High quality sequence stop: 403.
FEATURES Location/Qualifiers
source 1. .624
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3924266"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."
BASE COUNT 155 a 209 c 150 g 110 t
ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 624;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 gcgtttcgatgaaccc 20
||||||||||||||||
Db 582 GCGTTTCGATGAACCC 597

```
RESULT   4
BM077908
LOCUS       BM077908                384 bp    mRNA    linear   EST 14-NOV-2001
DEFINITION  pb21g06.y1 Ancylostoma caninum L3 SS SL1 TOPO v1 Murphy Chiapelli
            McCarter Ancylostoma caninum cDNA 5', mRNA sequence.
ACCESSION   BM077908
VERSION     BM077908.1  GI:16924944
KEYWORDS    EST.
SOURCE      dog hookworm.
  ORGANISM  Ancylostoma caninum
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
            Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
REFERENCE   1  (bases 1 to 384)
  AUTHORS   McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.
            , Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.
            , Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R.
            , Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
            ,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.
            , Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
            Wilson,R.
  TITLE     The Washington Univ. Nematode EST Project, 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: McCarter JP
            The Washington Univ. Nematode EST Project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            The library was constructed by Claire Murphy, Brandi Chiapelli, and
            Dr. James McCarter at Washington University, St. Louis. DNA
            Sequencing by: Washington University Genome Sequencing Center.
FEATURES             Location/Qualifiers
     source          1. .384
                     /organism="Ancylostoma caninum"
                     /db_xref="taxon:29170"
                     /clone_lib="Ancylostoma caninum L3 SS SL1 TOPO v1 Murphy
                     Chiapelli McCarter"
                     /dev_stage="Serum stimulated L3"
                     /lab_host="DH10B"
                     /note="Vector: pCRII-TOPO (Invitrogen); Site_1: EcoRI;
                     Site_2: EcoRI; The library was constructed by Claire
                     Murphy, Brandi Chiapelli,  and Dr. James McCarter at
                     Washington University, St. Louis. Oligo(dT)-SL1  PCR based
                     library. Ancylostoma caninum SS/L3 cDNA PCR products of
                     size  >400 nucleotides containing SL1 on the 5' end and
                     oligo(dT) on the 3' end  were non-directionally cloned
                     into pCRII-TOPO(Invitrogen) following the  Topo TA cloning
                     protocol. Nematodes were provided by Dr. Prema Arasu
                     (Prema_Arasu@ncsu.edu) of North Carolina State University
                     in Raleigh, NC."
BASE COUNT      116 a     71 c     85 g    112 t
ORIGIN


  Query Match             75.0%;  Score 15;  DB 10;  Length 384;
  Best Local Similarity   100.0%;  Pred. No. 39;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggcgtttcgatgaac 18
          ||||||||||||||||
Db    324 GGCGTTTCGATGAAC 338


RESULT   5
AW694629/c
LOCUS       AW694629                452 bp    mRNA    linear   EST 21-DEC-2000
DEFINITION  NF078E03ST1F1021 Developing stem Medicago truncatula cDNA clone
            NF078E03ST 5', mRNA sequence.
ACCESSION   AW694629
VERSION     AW694629.2  GI:11957636
KEYWORDS    EST.
SOURCE      barrel medic.
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 452)
  AUTHORS   He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
            ,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
            ,R.A.
  TITLE     Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula stem library
  JOURNAL   Unpublished (2000)
COMMENT     On Apr 14, 2000 this sequence version replaced gi:7569391.
            Contact: Dixon RA
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7302
            Fax: 580 221 7380
            Email: radixon@noble.org
            Insert Length: 736   Std Error: 0.00
            Plate: 078  row: E  column: 03
            Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
     source          1. .452
                     /organism="Medicago truncatula"
                     /db_xref="taxon:3880"
                     /clone="NF078E03ST"
                     /clone_lib="Developing stem"
                     /tissue_type="stem"
                     /dev_stage="Pooled developmental"
                     /note="Vector: Lambda Zap; Contains a mixture of
                     internodal stem segments"
BASE COUNT      152 a     94 c     91 g    115 t
ORIGIN


  Query Match             75.0%;  Score 15;  DB 9;  Length 452;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 cgtttcgatgaaccc 20
          |||||||||||||||
Db    338 CGTTTCGATGAACCC 324


RESULT   6
TA247H04P
LOCUS       TA247H04P               517 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 247h04, forward sequence,
            genomic survey sequence.
ACCESSION   AL483262
VERSION     AL483262.1  GI:11848938
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei.
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 517)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
```

4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

```
FEATURES             Location/Qualifiers
     source          1. .517
                     /organism="Trypanosoma brucei"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="247h04"
BASE COUNT      116 a    116 c    135 g    150 t
ORIGIN
```

```
  Query Match             75.0%;  Score 15;  DB 12;  Length 517;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggcgtttcgatgaac 18
          ||||||||||||||||
Db    293 GGCGTTTCGATGAAC 307
```

```
RESULT   7
AQ783856
LOCUS       AQ783856                536 bp    DNA     linear   GSS 03-AUG-1999
DEFINITION  HS_2001_A2_F09_T7C CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=2001 Col=18 Row=K, DNA sequence.
ACCESSION   AQ783856
VERSION     AQ783856.1  GI:5691480
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 536)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones may be purchased from Research Genetics (info@resgen.com).
            BAC end Web Server: http://www.htsc.washington.edu
            Plate: 2001  row: K  column: 18
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 536.
FEATURES             Location/Qualifiers
     source          1. .536
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=2001 Col=18 Row=K"
                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                     /sex="male"
                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                     E-Coli DH10B"
BASE COUNT      160 a    124 c     92 g    156 t      4 others
ORIGIN
```

```
  Query Match             75.0%;  Score 15;  DB 12;  Length 536;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 cgtttcgatgaaccc 20
          |||||||||||||||
Db    506 CGTTTCGATGAACCC 520
```

```
RESULT   8
TA140G03P
LOCUS       TA140G03P               537 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 140g03, forward sequence,
            genomic survey sequence.
ACCESSION   AL466454
VERSION     AL466454.1  GI:11835809
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei.
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 537)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .537
                     /organism="Trypanosoma brucei"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="140g03"
BASE COUNT      108 a    120 c    110 g    199 t
ORIGIN
```

```
  Query Match             75.0%;  Score 15;  DB 12;  Length 537;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggcgtttcgatgaac 18
          ||||||||||||||||
Db     85 GGCGTTTCGATGAAC 99
```

```
RESULT   9
TA190A10P/c
LOCUS       TA190A10P               540 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 190a10, forward sequence,
            genomic survey sequence.
ACCESSION   AL477985
VERSION     AL477985.1  GI:11841795
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei.
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
```

```
REFERENCE   1  (bases 1 to 540)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nhl@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .540
                     /organism="Trypanosoma brucei"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="190a10"
BASE COUNT      177 a    118 c    126 g    119 t
ORIGIN


  Query Match             75.0%;  Score 15;  DB 12;  Length 540;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggcgtttcgatgaac 18
          |||||||||||||||
Db    325 GGCGTTTCGATGAAC 311


RESULT  10
BH615799
LOCUS       BH615799                631 bp    DNA     linear   GSS 28-JAN-2002
DEFINITION  BMBAC304F01SP6_PSU Brugia malayi Genomic Bac Library 3 Brugia
            malayi genomic, DNA sequence.
ACCESSION   BH615799
VERSION     BH615799.1  GI:18380487
KEYWORDS    GSS.
SOURCE      Brugia malayi.
  ORGANISM  Brugia malayi
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Brugia.
REFERENCE   1  (bases 1 to 631)
  AUTHORS   Whitton,C., Daub,J., Ware,J., Quail,M., Hall,N., Barrell,B., Foster
            ,J., Guiliano,D., Slatko,B. and Blaxter,M.
  TITLE     Genome survey sequences from the human parasitic nematode Brugia
            malayi
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Blaxter ML
            Institute of Cell, Animal and Population Biology
            University of Edinburgh
            Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
            3JT, UK
            Tel: +44 131 650 6760
            Fax: +44 131 670 5450
            Email: mark.blaxter@ed.ac.uk
            Sequenced from the Brugia malayi BAC library constructed by Claire
            Whitton and Dr Mike Quail. The sequence was generated by The
            Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in
            collaboration with Mark Blaxter, ICAPB, University of Edinburgh,
            Edinburgh, UK.
            Seq primer: SP6 (ATTTAGGTGACACTATAG)
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .631
                     /organism="Brugia malayi"
                     /strain="TRS"
                     /db_xref="taxon:6279"
                     /clone_lib="Brugia malayi Genomic Bac Library 3"
                     /sex="Mixed (male and female)"
                     /tissue_type="whole parasite"
                     /dev_stage="microfilaria (L1)"
                     /note="Vector: pBACe3.6; Site_1: BamH I; Brugia malayi
                     genomic DNA was partially cleaved with Sau3A I and size
                     fractionated. 7,392 clones were generated with mean insert
                     size ~48 kbp. The library was constructed by Claire
                     Whitton, Blaxter Nematode Genetics Lab, University of
                     Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing
                     Unit, The Sanger Centre, Cambridge, UK."
BASE COUNT      196 a     94 c    142 g    199 t
ORIGIN


  Query Match             75.0%;  Score 15;  DB 12;  Length 631;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 acggcgtttcgatga 16
          |||||||||||||||
Db    606 ACGGCGTTTCGATGA 620


RESULT  11
BE053145
LOCUS       BE053145                690 bp    mRNA    linear   EST 07-MAR-2001
DEFINITION  GA__Ea0002K16f Gossypium arboreum 7-10 dpa fiber library Gossypium
            arboreum cDNA clone GA__Ea0002K16f, mRNA sequence.
ACCESSION   BE053145
VERSION     BE053145.2  GI:13244065
KEYWORDS    EST.
SOURCE      Gossypium arboreum.
  ORGANISM  Gossypium arboreum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
REFERENCE   1  (bases 1 to 690)
  AUTHORS   Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
            ,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
  TITLE     An integrated analysis of the genetics, development, and evolution
            of the cotton fiber
  JOURNAL   Unpublished (2000)
COMMENT     On Jun 8, 2000 this sequence version replaced gi:8380201.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Seq primer: TAATACGACTCACTATAGGG
            High quality sequence stop: 550.
FEATURES             Location/Qualifiers
     source          1. .690
                     /organism="Gossypium arboreum"
                     /strain="AKA"
                     /cultivar="8400"
                     /db_xref="taxon:29729"
                     /clone="GA__Ea0002K16f"
                     /clone_lib="Gossypium arboreum 7-10 dpa fiber library"
                     /tissue_type="Fibers isolated from bolls harvested 7-10
                     dpa"
                     /lab_host="E. coli"
                     /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT      169 a    132 c    151 g    236 t      2 others
ORIGIN
```

```
  Query Match             75.0%;  Score 15;  DB 9;  Length 690;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggcgtttcgatgaac 18
          ||||||||||||||||
Db    567 GGCGTTTCGATGAAC 581


RESULT  12
CNS040YP/c
LOCUS       CNS040YP                1033 bp    DNA     linear   GSS 18-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            073004 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL269530
VERSION     AL269530.1  GI:7991421
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 1033)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1033)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1033)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .1033
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="073004"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0BG073BH02LP1~end : T7"
BASE COUNT      270 a    222 c    276 g    261 t      4 others
ORIGIN


  Query Match             75.0%;  Score 15;  DB 12;  Length 1033;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 cggcgtttcgatgaa 17
          ||||||||||||||||
Db    460 CGGCGTTTCGATGAA 446


RESULT  13
BM007170
LOCUS       BM007170                1218 bp    mRNA    linear   EST 30-OCT-2001
DEFINITION  603614933T1 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:5420816 3',
            mRNA sequence.
ACCESSION   BM007170
VERSION     BM007170.1  GI:16521524
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1218)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1876  row: a  column: 09
            High quality sequence start: 25
            High quality sequence stop: 313.
FEATURES             Location/Qualifiers
     source          1. .1218
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5420816"
                     /clone_lib="NIH_MGC_110"
                     /tissue_type="ductal carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      370 a    446 c    244 g    154 t      4 others
ORIGIN


  Query Match             75.0%;  Score 15;  DB 10;  Length 1218;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 cgtttcgatgaaccc 20
          ||||||||||||||||
Db    364 CGTTTCGATGAACCC 378


RESULT  14
AV640031/c
LOCUS       AV640031                247 bp    mRNA    linear   EST 15-DEC-2000
DEFINITION  AV640031 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii
            cDNA clone HCL009b04_r 5', mRNA sequence.
ACCESSION   AV640031
VERSION     AV640031.1  GI:10783359
KEYWORDS    EST.
SOURCE      Chlamydomonas reinhardtii.
  ORGANISM  Chlamydomonas reinhardtii
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
            Chlamydomonadaceae; Chlamydomonas.
REFERENCE   1  (bases 1 to 247)
  AUTHORS   Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
            Nakamura,Y. and Tabata,S.
  TITLE     Generation of expressed sequence tags from low-CO2 and high-CO2
            adapted cells of Chlamydomonas reinhardtii
  JOURNAL   DNA Res. 7 (5), 305-307 (2000)
  MEDLINE   20539644
COMMENT     Contact: Erika Asamizu
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
```

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           Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
           Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES             Location/Qualifiers
     source          1. .247
                     /organism="Chlamydomonas reinhardtii"
                     /strain="C9"
                     /db_xref="taxon:3055"
                     /clone="HCL009b04_r"
                     /clone_lib="Chlamydomonas reinhardtii 5% CO2"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI; The cDNA library was constructed from cells cultured
                     in a medium with bubbling air containing 5% carbon
                     dioxide"
BASE COUNT       61 a     79 c     54 g     53 t
ORIGIN


  Query Match           70.0%;  Score 14;  DB 9;  Length 247;
  Best Local Similarity  100.0%;  Pred. No. 1.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggcgtttcgatgaa 17
          ||||||||||||||
Db    245 GGCGTTTCGATGAA 232


RESULT 15
AV640876/c
LOCUS       AV640876                269 bp    mRNA    linear   EST 15-DEC-2000
DEFINITION  AV640876 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii
            cDNA clone HCL024a01_r 5', mRNA sequence.
ACCESSION   AV640876
VERSION     AV640876.1  GI:10784204
KEYWORDS    EST.
SOURCE      Chlamydomonas reinhardtii.
  ORGANISM  Chlamydomonas reinhardtii
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
            Chlamydomonadaceae; Chlamydomonas.
REFERENCE   1  (bases 1 to 269)
  AUTHORS   Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
            Nakamura,Y. and Tabata,S.
  TITLE     Generation of expressed sequence tags from low-CO2 and high-CO2
            adapted cells of Chlamydomonas reinhardtii
  JOURNAL   DNA Res. 7 (5), 305-307 (2000)
  MEDLINE   20539644
COMMENT     Contact: Erika Asamizu
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES             Location/Qualifiers
     source          1. .269
                     /organism="Chlamydomonas reinhardtii"
                     /strain="C9"
                     /db_xref="taxon:3055"
                     /clone="HCL024a01_r"
                     /clone_lib="Chlamydomonas reinhardtii 5% CO2"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI; The cDNA library was constructed from cells cultured
                     in a medium with bubbling air containing 5% carbon
                     dioxide"
BASE COUNT       65 a     85 c     60 g     59 t
ORIGIN


  Query Match           70.0%;  Score 14;  DB 9;  Length 269;
  Best Local Similarity  100.0%;  Pred. No. 1.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggcgtttcgatgaa 17
          ||||||||||||||
Db    254 GGCGTTTCGATGAA 241
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Search completed: August 7, 2002, 23:12:33
Job time: 11072 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 8, 2002, 00:01:21 ; Search time 562.71 Seconds
(without alignments)
61.023 Million cell updates/sec

Title: US-09-786-105-2
Perfect score: 20
Sequence: 1 tacggcgtttcgatgaaccc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_032802:*
1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
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12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
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20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	21	AAA49824	Mycobacterium tube
	2	20	100.0	20	21	AAA49826	Mycobacterium tube
c	3	20	100.0	432	14	AAQ61457	M.tuberculosis rpo
c	4	20	100.0	480	21	AAA49863	Mycobacterium tube
c	5	20	100.0	620	17	AAT29126	rpoB gene fragment
c	6	20	100.0	620	17	AAT29124	rpoB gene fragment
c	7	20	100.0	620	17	AAT29125	rpoB gene fragment
c	8	20	100.0	970	17	AAT09676	Mycobacterium tube
c	9	20	100.0	3519	22	AAH51976	Mycobacterium tube
c	10	20	100.0	3534	22	AAH02079	Mycobacterium tube
c	11	20	100.0	3853	21	AAA74651	Mycobacterium tube
c	12	20	100.0	3853	21	AAA89994	M. tuberculosis rp
	13	19	95.0	19	17	AAT12096	M. tuberculosis rp
	14	15	75.0	27	17	AAT09670	Mycobacterium tube
c	15	14	70.0	3447	14	AAQ51532	M.leprae rpoB gene
c	16	14	70.0	3474	23	AAS51357	Enterococcus faeca
c	17	14	70.0	3624	23	AAS52892	Enterococcus faeca
	18	14	70.0	6275	24	ABL32551	Human immune syste
	19	14	70.0	6319	23	ABL18447	Drosophila melanog
	20	14	70.0	9179	20	AAX13246	Enterococcus faeca
	21	14	70.0	9728	24	ABL33903	Human immune syste
	22	14	70.0	29555	23	ABL18446	Drosophila melanog
	23	13	65.0	58	22	AAF61643	Lactobacillus case
	24	13	65.0	234	17	AAT13651	AcNPV ORF 43, resi
	25	13	65.0	351	22	AAF61568	Lactobacillus case
	26	13	65.0	383	19	AAV04618	Flea aminopeptidas
	27	13	65.0	383	22	AAC90900	Flea aminopeptidas
c	28	13	65.0	421	23	AAS94185	DNA encoding novel
	29	13	65.0	537	19	AAV04619	Flea aminopeptidas
	30	13	65.0	537	22	AAC90901	Flea aminopeptidas
	31	13	65.0	667	22	AAF71326	Corynebacterium gl
c	32	13	65.0	1086	22	AAF27618	Mevalonate pathway
c	33	13	65.0	1227	23	AAS87269	DNA encoding novel
	34	13	65.0	1242	23	ABL22843	Drosophila melanog
c	35	13	65.0	1261	18	AAV74720	Staphylococcus aur
	36	13	65.0	1326	22	AAH68314	C glutamicum codin
c	37	13	65.0	1407	22	AAH53127	S. epidermidis ope
c	38	13	65.0	1473	21	AAC48699	Arabidopsis thalia
c	39	13	65.0	1475	21	AAC32775	Arabidopsis thalia
	40	13	65.0	1938	22	AAF89013	Murine FATP1 codin
	41	13	65.0	2109	23	AAS92952	DNA encoding novel
c	42	13	65.0	2192	23	AAS92789	DNA encoding novel
	43	13	65.0	2222	20	AAZ38124	Human FATP variant
	44	13	65.0	2470	23	AAS94186	DNA encoding novel
c	45	13	65.0	2870	23	ABL26802	Drosophila melanog

ALIGNMENTS

RESULT 1
AAA49824
ID AAA49824 standard; DNA; 20 BP.
XX
AC AAA49824;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene amplification primer rpoB-R.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX

PS Claim 4; Page 4; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene amplification primer rpoB-R (bp
CC 2611-2592). It is used with the forward primer given in AAA49823
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 1 tacggcgtttcgatgaaccc 20

RESULT 2
AAA49826
ID AAA49826 standard; DNA; 20 BP.
XX
AC AAA49826;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-3s.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene sequencing primer rpoB-3s (bp
CC 2611-2592). It is used with the forward primer given in AAA49825 and
CC with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 1 tacggcgtttcgatgaaccc 20

RESULT 3
AAQ61457/c
ID AAQ61457 standard; DNA; 432 BP.
XX
AC AAQ61457;
XX
DT 17-MAY-1994 (first entry)
XX
DE M.tuberculosis rpoB gene fragment.
XX
KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KW mutant; ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9322454-A.
XX
PD 11-NOV-1993.
XX
PF 30-APR-1993; 93WO-EP01063.
XX
PR 17-SEP-1992; 92FR-0011098.
PR 30-APR-1992; 92US-0875940.
PR 14-AUG-1992; 92US-0929206.
PR 16-APR-1993; 93FR-0004545.
XX
PA (ASSI-) ASSISTANCE PUBLIQUE.
PA (INSP) INST PASTEUR.
PA (MEDI-) MEDICAL RES COUNCIL.
PA (UYBE-) UNIV BERNE.
PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
PI Young D, Zhang Y;
XX
DR WPI; 1993-368812/46.
DR P-PSDB; AAR51372.
XX

PT Rapid detection of antibiotic resistance in Mycobacteria - esp.
PT isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in katG, rpoB or rpsL genes
XX
PS Example 2; Fig 13; 97pp; English.
XX
CC PCR amplification was used to obtain rpoB genes from rifampicin-
CC resistant Mycobacterium leprae strains. A comparison with the
CC sequence of the rpoB gene from sensitive strains (AAQ51532) revealed
CC mutations in the region encoding amino acids 400-450. The corresp.
CC region was isolated from M.tuberculosis (AAQ61457). A common
CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
SQ Sequence 432 BP; 78 A; 139 C; 148 G; 67 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 428 TACGGCGTTTCGATGAACCC 409

RESULT 4
AAA49863/c
ID AAA49863 standard; DNA; 480 BP.
XX
AC AAA49863;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene (rifampin resistance).
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; ss.
XX
OS Mycobacterium tuberculosis.
XX
FH Key Location/Qualifiers
FT primer_bind complement(41..60)
FT /*tag= a
FT /note= "primer of AAA49823"
FT primer_bind 372..391
FT /*tag= b
FT /note= "primer of AAA49824"
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Disclosure; Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene (bp2161-2640). Amplification and
CC cycle sequencing primers (see AAA49823-62) are used for the detection
CC and analysis of antibiotic resistance-associated mutations in
CC defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 0.0075;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 451 TACGGCGTTTCGATGAACCC 432

RESULT 5
AAT29126/c
ID AAT29126 standard; DNA; 620 BP.
XX
AC AAT29126;
XX
DT 02-DEC-1996 (first entry)
XX
DE rpoB gene fragment (mutant) from Mycobacterium tuberculosis.
XX
KW p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus;
KW Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
KW Staphylococcus; identification; detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US14673.
XX
PR 30-AUG-1995; 95US-0520946.
PR 09-NOV-1994; 94US-0337164.
PR 09-MAR-1995; 95US-0402601.
PR 07-JUN-1995; 95US-0484956.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM;
XX
DR WPI; 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
PS Example 33; Page 306; 433pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene; for
CC identifying strains of microorganisms, especially bacteria selected
CC from the the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the Mycobacterium tuberculosis rpoB gene, which, when
CC mutated is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451Y and S456L mutations. The amplified
CC fragments are given in AAT29124 (Wild type) and AAT29125-26
CC (mutant sequences).
XX
SQ Sequence 620 BP; 103 A; 201 C; 214 G; 102 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
AAT29124/c
ID AAT29124 standard; DNA; 620 BP.
XX
AC AAT29124;
XX
DT 02-DEC-1996 (first entry)
XX
DE rpoB gene fragment from Mycobacterium tuberculosis.
XX
KW p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus;
KW Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
KW Staphylococcus; identification; detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US14673.
XX
PR 30-AUG-1995; 95US-0520946.
PR 09-NOV-1994; 94US-0337164.
PR 09-MAR-1995; 95US-0402601.
PR 07-JUN-1995; 95US-0484956.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM;
XX
DR WPI; 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
PS Example 33; Page 305; 433pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene; for
CC identifying strains of microorganisms, especially bacteria selected
CC from the the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the Mycobacterium tuberculosis rpoB gene, which, when
CC mutated is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451Y and S456L mutations. The amplified
CC fragments are given in AAT29124 (Wild type) and AAT29125-26
CC (mutant sequences).
XX
SQ Sequence 620 BP; 103 A; 202 C; 214 G; 101 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 7
AAT29125/c
ID AAT29125 standard; DNA; 620 BP.
XX
AC AAT29125;
XX
DT 02-DEC-1996 (first entry)
XX
DE rpoB gene fragment (mutant) from Mycobacterium tuberculosis.
XX
KW p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus;
KW Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
KW Staphylococcus; identification; detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US14673.
XX
PR 30-AUG-1995; 95US-0520946.
PR 09-NOV-1994; 94US-0337164.
PR 09-MAR-1995; 95US-0402601.
PR 07-JUN-1995; 95US-0484956.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM;
XX
DR WPI; 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
PS Example 33; Page 305-306; 433pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

```
CC   compared to the cleavage products of reference gene sequences.  The
CC   method is used for detecting mutation in the human p53 gene; for
CC   identifying strains of microorganisms, especially bacteria selected
CC   from the the group of members of the genera Campylobacter,
CC   Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC   The method may also be used for the identification of viruses,
CC   especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC   (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC   region of the Mycobacterium tuberculosis rpoB gene, which, when
CC   mutated is associated with rifampin resistance. The 620 bp region
CC   amplified spans both the H451Y and S456L mutations.  The amplified
CC   fragments are given in AAT29124 (Wild type) and AAT29125-26
CC   (mutant sequences).
XX
SQ   Sequence 620 BP; 103 A; 201 C; 214 G; 102 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 17;  Length 620;
  Best Local Similarity   100.0%;  Pred. No. 0.0073;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    296 TACGGCGTTTCGATGAACCC 277


RESULT   8
AAT09676/c
ID   AAT09676 standard; DNA; 970 BP.
XX
AC   AAT09676;
XX
DT   15-OCT-1996  (first entry)
XX
DE   Mycobacterium tuberculosis rpoB gene DNA sequence.
XX
KW   Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;
KW   polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.
XX
OS   Mycobacterium tuberculosis.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     10..27
FT                   /*tag=  a
FT                   /note= "primer FENLFF"
FT   primer_bind     226..243
FT                   /*tag=  b
FT                   /note= "primer DDIDHL"
FT   primer_bind     226..240
FT                   /*tag=  c
FT                   /note= "primer DDIDH"
FT   primer_bind     338..364
FT                   /*tag=  d
FT                   /note= "primer rpo95"
FT   primer_bind     348..373
FT                   /*tag=  e
FT                   /note= "primer rpo105"
FT   primer_bind     354..373
FT                   /*tag=  f
FT                   /note= "primer KY290"
FT   misc_feature    372..373
FT                   /*tag=  g
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    433..434
FT                   /*tag=  h
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    438
FT                   /*tag=  i
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    468..469
FT                   /*tag=  j
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    486
FT                   /*tag=  k
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    501
FT                   /*tag=  l
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    516
FT                   /*tag=  m
FT                   /note= "M. tuberculosis signature nucleotide"
FT   primer_bind     516..535
FT                   /*tag=  n
FT                   /note= "primer rpo273"
FT   misc_feature    525
FT                   /*tag=  o
FT                   /note= "M. tuberculosis signature nucleotide"
FT   primer_bind     525..541
FT                   /*tag=  p
FT                   /note= "primer KY292"
FT   primer_bind     536..562
FT                   /*tag=  q
FT                   /note= "primer rpo293"
FT   primer_bind     640..666
FT                   /*tag=  r
FT                   /note= "primer rpo397"
FT   primer_bind     952..966
FT                   /*tag=  s
FT                   /note= "primer NMQRQ-1"
FT   primer_bind     952..966
FT                   /*tag=  t
FT                   /note= "primer NMQRQ-2"
XX
PN   WO9533074-A1.
XX
PD   07-DEC-1995.
XX
PF   26-MAY-1995;   95WO-US06790.
XX
PR   26-MAY-1994;   94US-0250030.
XX
PA   (HOFF ) HOFFMANN LA ROCHE INC.
PA   (MAYO-) MAYO FOUNDATION.
XX
PI   Felmlee TA,  Hunt JM,  Persing DH,  Roberts GD,  Whelen AC;
PI   Young KKY;
XX
DR   WPI; 1996-030581/03.
XX
PT   Detection of Mycobacterium tuberculosis - by amplifying sample DNA
PT   with a primer set that targets portions of the gene encoding rpoB.
XX
PS   Disclosure; Fig.3; 54pp; English.
XX
CC   This oligonucleotide DNA primer is specific for Mycobacterium
CC   tuberculosis, and may be used to amplify a sample DNA by targeting
CC   a portion of the gene encoding rpoB.  The 1st several bases comprise a
CC   nonhybridizing tail consisting of filler bases followed by
CC   a restriction site incorporated to facilitate cloning using the
CC   amplicon at a later date, if desired.  The remaining bases hybridize
CC   to bacterial rpoB DNA.  The method provides for the detection of M.
CC   tuberculosis and the concurrent determination of its drug
CC   susceptibility, particularly to rifamycin.  The method can provide
CC   often greater than 95% sensitivity and 100% specificity.  The
CC   biological sample is a fluid or tissue sample from a human.
XX
SQ   Sequence 970 BP; 182 A; 302 C; 330 G; 156 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 17;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 0.0071;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    671 TACGGCGTTTCGATGAACCC 652
```

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RESULT   9
AAH51976/c
ID   AAH51976 standard; DNA; 3519 BP.
XX
AC   AAH51976;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Mycobacterium tuberculosis potential drug target gene SEQ ID 30.
XX
KW   Drug target; growth; organism viability; characterisation; ds.
XX
OS   Mycobacterium tuberculosis.
XX
PN   WO200135317-A1.
XX
PD   17-MAY-2001.
XX
PF   13-NOV-2000; 2000WO-US31152.
XX
PR   12-NOV-1999;   99US-0165086.
PR   12-NOV-1999;   99US-0165124.
PR   01-FEB-2000; 2000US-0179531.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Eisenberg D,  Rotstein SH,  Marcotte EM;
XX
DR   WPI; 2001-329193/34.
DR   P-PSDB; AAG81125.
XX
PT   Identifying nucleotide or polypeptide sequence for use as drug target,
PT   involves providing algorithm that analyzes a functional relationship
PT   between nucleotide or polypeptide sequences, and comparing the
PT   sequences  -
XX
PS   Disclosure; Page 68-69; 207pp; English.
XX
CC   This invention relates to a method for identifying a nucleotide or
CC   polypeptide sequence that may be a drug target, or essential for growth
CC   or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
CC   represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
CC   tuberculosis proteins which are potential drug targets. The DNA and
CC   protein sequences are used to illustrate the method of the invention. The
CC   method involves providing an unknown nucleotide or polypeptide sequences,
CC   and comparing it to a number of sequences along with at least one
CC   algorithm capable of analysing a functional relationship between
CC   nucleotide and polypeptide sequences. The method is useful for
CC   characterising the function of nucleic acids and polypeptides that may be
CC   useful as a target for a drug or essential for the growth or viability of
CC   an organism.
XX
SQ   Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 22;  Length 3519;
  Best Local Similarity   100.0%;  Pred. No. 0.0064;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
           ||||||||||||||||||||
Db    1529 TACGGCGTTTCGATGAACCC 1510


RESULT  10
AAH02079/c
ID   AAH02079 standard; DNA; 3534 BP.
XX
AC   AAH02079;
XX
DT   24-JUL-2001  (first entry)
XX
DE   Mycobacterium tuberculosis nucleotide sequence SEQ ID NO:2072.
XX
KW   Species specific; genus specific; family specific; probe; detection;
KW   identification; algal; archaeal; bacterial; fungal; parasitical;
KW   microorganism; diagnosis; translation elongation factor Tu; toxin;
KW   translation elongation factor G; RecA recombinase; resistance;
KW   catalytic subunit of proton-translocating ATPase; antimicrobial;
KW   vaccine; primer; ds.
XX
OS   Mycobacterium tuberculosis.
XX
PN   WO200123604-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-CA01150.
XX
PR   28-SEP-1999;   99CA-2283458.
PR   19-MAY-2000; 2000CA-2307010.
XX
PA   (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI   Bergeron MG,  Boissinot M,  Huletsky A,  Menard C,  Ouellette M;
PI   Picard FJ,  Roy PH;
XX
DR   WPI; 2001-245006/25.
XX
PT   Nucleic acid sequences are used to generate universal probes and
PT   primers which can be used to identify and detect the presence of algal,
PT   archaeal, bacterial, fungal and parasitical species in a test sample -
XX
PS   Disclosure; Page 1478-1479; 1580pp; English.
XX
CC   The present invention describes a method for generating a repertory of
CC   nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC   and/or primers are derived. The method comprises amplifying the nucleic
CC   acids of determined algal, archaeal, bacterial, fungal and parasitical
CC   species with a combination of defined primer pairs. The method can be
CC   used for producing probes and/or primers for detecting one or more
CC   related microorganisms e.g. algae, archaea, bacteria, fungi and
CC   parasites, for universal detection and for specific and ubiquitous
CC   detection and identification of an algal, archaeal, bacterial, fungal
CC   and parasitical species, genus, family and group. A nucleic acid (I)
CC   obtained using the method of the invention can be used for the universal
CC   detection of any bacterium, fungus or parasite in a sample and for the
CC   detection of at least one antimicrobial agent resistance gene or at
CC   least one toxin gene. hexA nucleic acids are used for the specific and
CC   ubiquitous detection and for identification of Streptococcus pneumoniae.
CC   (I) can be used to design a therapeutic agent which is effective against
CC   microorganisms. Microbial species or genus or family or phylum or group
CC   which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC   Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC   Mycobacteriaceae family, Pseudomonads group, Streptococcus sp.,
CC   Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests
CC   provides faster results than substrate specificity tests as results can
CC   be determined in an hour and improved accuracy is also achieved.
CC   AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
CC   which are given in the exemplification of the present invention.
XX
SQ   Sequence 3534 BP; 679 A; 1081 C; 1188 G; 586 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 22;  Length 3534;
  Best Local Similarity   100.0%;  Pred. No. 0.0064;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
           ||||||||||||||||||||
Db    1547 TACGGCGTTTCGATGAACCC 1528


RESULT  11
```

AAA74651/c
ID AAA74651 standard; DNA; 3853 BP.
XX
AC AAA74651;
XX
DT 06-DEC-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene.
XX
KW Mycobacterium tuberculosis; rpoB; RNA polymerase beta subunit;
KW rifampin resistance; mutation detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200043546-A2.
XX
PD 27-JUL-2000.
XX
PF 20-DEC-1999; 99WO-US30377.
XX
PR 19-JAN-1999; 99US-0233996.
XX
PA (DADE-) DADE BEHRING INC.
XX
PI Liu YP, Kurn N;
XX
DR WPI; 2000-524243/47.
XX
PT Method for detecting drug resistance in a strain of an organism,
PT particularly for detecting rifampin resistance in Mycobacterium
PT tuberculosis -
XX
PS Example 1; Fig 4; 86pp; English.
XX
CC The present sequence is the rpoB gene from Mycobacterium tuberculosis.
CC Rifampin resistance is largely associated with point mutations
CC localised in a small core region of 81 base pairs in the rpoB gene, which
CC encodes the RNA polymerase beta subunit. To detect a mutation, a complex
CC is formed comprising a first sequence representing the predetermined
CC region of the gene of the organism and a second sequence representing the
CC corresponding region of the gene of the wild type organism in double
CC stranded form. Each member of at least one pair of non-complementary
CC strands within the complex has a label. The association of the labels in
CC the complex is related to the presence of the mutation. The presence of
CC the mutation is related to the drug resistance of the strain.
XX
SQ Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 2122 TACGGCGTTTCGATGAACCC 2103

RESULT 12
AAA89994/c
ID AAA89994 standard; DNA; 3853 BP.
XX
AC AAA89994;
XX
DT 18-DEC-2000 (first entry)
XX
DE M. tuberculosis rpoB gene encoding RNA polymerase beta subunit.
XX
KW Drug resistance; rifampin; rifampicin; pyrazinamide; rpoB;
KW RNA polymerase beta subunit; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200043545-A2.
XX
PD 27-JUL-2000.
XX
PF 14-DEC-1999; 99WO-US29517.
XX
PR 19-JAN-1999; 99US-0233996.
PR 22-APR-1999; 99US-0296894.
XX
PA (DADE-) DADE BEHRING INC.
XX
PI Liu YP, Kurn N;
XX
DR WPI; 2000-499235/44.
XX
PT Detecting resistance of drugs such as rifampicin in strains of
PT Mycobacterium, comprising detecting mutations in a gene and relating
PT them to drug resistance -
XX
PS Example 1; Fig 4; 91pp; English.
XX
CC This invention relates to a method for detecting drug resistance in a
CC strain of an organism. The method comprises detecting the presence of at
CC least 1 mutation in a first sequence and relating the presence of the
CC mutation to drug resistance. Included in the invention are a kit for
CC carrying out the method and a method for detecting the presence of a
CC difference between two related nucleic acid sequences in an organism. The
CC methods are useful for detecting resistance to drugs such rifampin and
CC pyrazinamide in Mycobacterium. The present sequence represents the
CC Mycobacterium tuberculosis rpoB gene (which encodes the RNA polymerase
CC beta subunit). The sequence is used in an example of the method of the
CC invention for the detection of rifampin resistance in M. tuberculosis.
XX
SQ Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 2122 TACGGCGTTTCGATGAACCC 2103

RESULT 13
AAT12096
ID AAT12096 standard; DNA; 19 BP.
XX
AC AAT12096;
XX
DT 10-JUL-1996 (first entry)
XX
DE M. tuberculosis rpoB gene fragment amplification primer P6.
XX
KW Antibiotic; resistance; spectrum; gene; mycobacterium;
KW determination; amplification; tuberculosis; rpoB; fragment;
KW primer; differential; hybridisation; pattern; rifampicin;
KW rifabutin; species identification; ss.
XX
OS Synthetic.
XX
PN WO9533851-A2.
XX
PD 14-DEC-1995.
XX
PF 09-JUN-1995; 95WO-EP02230.
XX
PR 09-JUN-1994; 94EP-0870093.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI De Beenhouwer H, Jannes G, Machtelinckx L, Portaels F;

```
PI   Rossau R;
XX
DR   WPI; 1996-040250/04.
XX
PT   Probes and primers for determn. of antibiotic resistance spectrum of
PT   Mycobacterium, opt. coupled with species identification - from
PT   different patterns of hybridisation with rpoB gene
XX
PS   Claim 22; Page 39; 69pp; English.
XX
CC   The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC   determined by amplifying the relevant part of the antibiotic
CC   resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC   amplified using the primer set AAT12091-98, hybridising it with at
CC   least 1 rpoB gene probe, detecting the hybrids formed and
CC   inferring the ARS, and opt. the spp., from the differential
CC   hybridisation patterns. The method is partic. useful for the
CC   detection of rifampicin and/or rifabutin resistance in M. leprae
CC   or M. tuberculosis, and mycobacterial spp. identification. The
CC   method is rapid and reliable and provides simultaneous determn.
CC   of ARS and spp. identity.
XX
SQ   Sequence 19 BP; 4 A; 5 C; 5 G; 5 T; 0 other;


  Query Match             95.0%;  Score 19;  DB 17;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0.038;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaacc 19
          |||||||||||||||||||
Db      1 tacggcgtttcgatgaacc 19


RESULT  14
AAT09670
ID   AAT09670 standard; DNA; 27 BP.
XX
AC   AAT09670;
XX
DT   15-OCT-1996  (first entry)
XX
DE   Mycobacterium tuberculosis 27-mer oligonucleotide DNA primer rpo397.
XX
KW   Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;
KW   polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.
XX
OS   Synthetic.
XX
PN   WO9533074-A1.
XX
PD   07-DEC-1995.
XX
PF   26-MAY-1995;   95WO-US06790.
XX
PR   26-MAY-1994;   94US-0250030.
XX
PA   (HOFF ) HOFFMANN LA ROCHE INC.
PA   (MAYO-) MAYO FOUNDATION.
XX
PI   Felmlee TA,  Hunt JM,  Persing DH,  Roberts GD,  Whelen AC;
PI   Young KKY;
XX
DR   WPI; 1996-030581/03.
XX
PT   Detection of Mycobacterium tuberculosis - by amplifying sample DNA
PT   with a primer set that targets portions of the gene encoding rpoB.
XX
PS   Claim 9; Page 39; 54pp; English.
XX
CC   This oligonucleotide DNA primer is specific for Mycobacterium
CC   tuberculosis, and may be used to amplify a sample DNA by targeting
CC   a portion of the gene encoding rpoB.  The method provides for the
CC   detection of M. tuberculosis and the concurrent determination of its
CC   drug susceptibility, particularly to rifamycin.  The method can
CC   provide often greater than 95% sensitivity and 100% specificity.
CC   The biological sample is a fluid or tissue sample from a human.
XX
SQ   Sequence 27 BP; 6 A; 7 C; 8 G; 6 T; 0 other;


  Query Match             75.0%;  Score 15;  DB 17;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 8.8;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 cgtttcgatgaaccc 20
          |||||||||||||||
Db      1 cgtttcgatgaaccc 15


RESULT  15
AAQ51532/c
ID   AAQ51532 standard; DNA; 3447 BP.
XX
AC   AAQ51532;
XX
DT   17-MAY-1994  (first entry)
XX
DE   M.leprae rpoB gene.
XX
KW   rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KW   mutant; ss.
XX
OS   Mycobacterium leprae.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..3447
FT                   /*tag=  a
FT                   /note= "rifampicin-sensitive; in resistant
FT                          strains the Ser codon (TCG at
FT                          nucleotides 1273-1275) is often mutated
FT                          to a Phe, Met or esp. Leu codon"
XX
PN   WO9322454-A.
XX
PD   11-NOV-1993.
XX
PF   30-APR-1993;   93WO-EP01063.
XX
PR   17-SEP-1992;   92FR-0011098.
PR   30-APR-1992;   92US-0875940.
PR   14-AUG-1992;   92US-0929206.
PR   16-APR-1993;   93FR-0004545.
XX
PA   (ASSI-) ASSISTANCE PUBLIQUE.
PA   (INSP ) INST PASTEUR.
PA   (MEDI-) MEDICAL RES COUNCIL.
PA   (UYBE-) UNIV BERNE.
PA   (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI   Bodmer T,  Cole S,  Heym B,  Honore N,  Telenti A;
PI   Young D,  Zhang Y;
XX
DR   WPI; 1993-368812/46.
DR   P-PSDB; AAR43671.
XX
PT   Rapid detection of antibiotic resistance in Mycobacteria - esp.
PT   isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT   by detecting mutation in katG, rpoB or rpsL genes
XX
PS   Example 2; Fig 12; 97pp; English.
XX
CC   PCR amplification was used to obtain rpoB genes from rifampicin-
CC   resistant Mycobacterium leprae strains. A comparison with the
CC   sequence of the rpoB gene from sensitive strains (AAQ51532) revealed
CC   mutations in the region encoding amino acids 400-450. A common
```

CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
SQ Sequence 3447 BP; 687 A; 965 C; 1139 G; 656 T; 0 other;

Query Match 70.0%; Score 14; DB 14; Length 3447;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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           ||||||||||||||
Db    1448 GTTTCGATGAACCC 1435
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Search completed: August 8, 2002, 00:01:22
Job time: 7611 sec

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene; for
CC identifying strains of microorganisms, especially bacteria selected
CC from the the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the Mycobacterium tuberculosis rpoB gene, which, when
CC mutated is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451Y and S456L mutations. The amplified
CC fragments are given in AAT29124 (Wild type) and AAT29125-26
CC (mutant sequences).
XX
SQ Sequence 620 BP; 103 A; 201 C; 214 G; 102 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
AAT29124/c
ID AAT29124 standard; DNA; 620 BP.
XX
AC AAT29124;
XX
DT 02-DEC-1996 (first entry)
XX
DE rpoB gene fragment from Mycobacterium tuberculosis.
XX
KW p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus;
KW Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
KW Staphylococcus; identification; detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US14673.
XX
PR 30-AUG-1995; 95US-0520946.
PR 09-NOV-1994; 94US-0337164.
PR 09-MAR-1995; 95US-0402601.
PR 07-JUN-1995; 95US-0484956.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM;
XX
DR WPI; 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
PS Example 33; Page 305; 433pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene; for
CC identifying strains of microorganisms, especially bacteria selected
CC from the the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the Mycobacterium tuberculosis rpoB gene, which, when
CC mutated is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451Y and S456L mutations. The amplified
CC fragments are given in AAT29124 (Wild type) and AAT29125-26
CC (mutant sequences).
XX
SQ Sequence 620 BP; 103 A; 202 C; 214 G; 101 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 7
AAT29125/c
ID AAT29125 standard; DNA; 620 BP.
XX
AC AAT29125;
XX
DT 02-DEC-1996 (first entry)
XX
DE rpoB gene fragment (mutant) from Mycobacterium tuberculosis.
XX
KW p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus;
KW Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
KW Staphylococcus; identification; detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US14673.
XX
PR 30-AUG-1995; 95US-0520946.
PR 09-NOV-1994; 94US-0337164.
PR 09-MAR-1995; 95US-0402601.
PR 07-JUN-1995; 95US-0484956.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM;
XX
DR WPI; 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
PS Example 33; Page 305-306; 433pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

PT Rapid detection of antibiotic resistance in Mycobacteria - esp.
PT isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in katG, rpoB or rpsL genes
XX
PS Example 2; Fig 13; 97pp; English.
XX
CC PCR amplification was used to obtain rpoB genes from rifampicin-
CC resistant Mycobacterium leprae strains. A comparison with the
CC sequence of the rpoB gene from sensitive strains (AAQ51532) revealed
CC mutations in the region encoding amino acids 400-450. The corresp.
CC region was isolated from M.tuberculosis (AAQ61457). A common
CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
SQ Sequence 432 BP; 78 A; 139 C; 148 G; 67 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 428 TACGGCGTTTCGATGAACCC 409

RESULT 4
AAA49863/c
ID AAA49863 standard; DNA; 480 BP.
XX
AC AAA49863;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene (rifampin resistance).
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; ss.
XX
OS Mycobacterium tuberculosis.
XX
FH Key Location/Qualifiers
FT primer_bind complement(41..60)
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FT /note= "primer of AAA49823"
FT primer_bind 372..391
FT /*tag= b
FT /note= "primer of AAA49824"
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Disclosure; Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene (bp2161-2640). Amplification and
CC cycle sequencing primers (see AAA49823-62) are used for the detection
CC and analysis of antibiotic resistance-associated mutations in
CC defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 0.0075;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 451 TACGGCGTTTCGATGAACCC 432

RESULT 5
AAT29126/c
ID AAT29126 standard; DNA; 620 BP.
XX
AC AAT29126;
XX
DT 02-DEC-1996 (first entry)
XX
DE rpoB gene fragment (mutant) from Mycobacterium tuberculosis.
XX
KW p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus;
KW Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
KW Staphylococcus; identification; detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US14673.
XX
PR 30-AUG-1995; 95US-0520946.
PR 09-NOV-1994; 94US-0337164.
PR 09-MAR-1995; 95US-0402601.
PR 07-JUN-1995; 95US-0484956.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM;
XX
DR WPI; 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
PS Example 33; Page 306; 433pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

PS Claim 4; Page 4; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene amplification primer rpoB-R (bp
CC 2611-2592). It is used with the forward primer given in AAA49823
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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||||||||||||||||||||
Db 1 tacggcgtttcgatgaaccc 20

RESULT 2
AAA49826
ID AAA49826 standard; DNA; 20 BP.
XX
AC AAA49826;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-3s.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene sequencing primer rpoB-3s (bp
CC 2611-2592). It is used with the forward primer given in AAA49825 and
CC with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 1 tacggcgtttcgatgaaccc 20

RESULT 3
AAQ61457/c
ID AAQ61457 standard; DNA; 432 BP.
XX
AC AAQ61457;
XX
DT 17-MAY-1994 (first entry)
XX
DE M.tuberculosis rpoB gene fragment.
XX
KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KW mutant; ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9322454-A.
XX
PD 11-NOV-1993.
XX
PF 30-APR-1993; 93WO-EP01063.
XX
PR 17-SEP-1992; 92FR-0011098.
PR 30-APR-1992; 92US-0875940.
PR 14-AUG-1992; 92US-0929206.
PR 16-APR-1993; 93FR-0004545.
XX
PA (ASSI-) ASSISTANCE PUBLIQUE.
PA (INSP) INST PASTEUR.
PA (MEDI-) MEDICAL RES COUNCIL.
PA (UYBE-) UNIV BERNE.
PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
PI Young D, Zhang Y;
XX
DR WPI; 1993-368812/46.
DR P-PSDB; AAR51372.
XX

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 8, 2002, 00:01:25 ; Search time 562.71 Seconds
(without alignments)
61.023 Million cell updates/sec

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	21	AAA49824	Mycobacterium tube
	2	20	100.0	20	21	AAA49826	Mycobacterium tube
c	3	20	100.0	432	14	AAQ61457	M.tuberculosis rpo
c	4	20	100.0	480	21	AAA49863	Mycobacterium tube
c	5	20	100.0	620	17	AAT29126	rpoB gene fragment
c	6	20	100.0	620	17	AAT29124	rpoB gene fragment
c	7	20	100.0	620	17	AAT29125	rpoB gene fragment
c	8	20	100.0	970	17	AAT09676	Mycobacterium tube
c	9	20	100.0	3519	22	AAH51976	Mycobacterium tube
c	10	20	100.0	3534	22	AAH02079	Mycobacterium tube
c	11	20	100.0	3853	21	AAA74651	Mycobacterium tube
c	12	20	100.0	3853	21	AAA89994	M. tuberculosis rp
	13	19	95.0	19	17	AAT12096	M. tuberculosis rp
	14	15	75.0	27	17	AAT09670	Mycobacterium tube
c	15	14	70.0	3447	14	AAQ51532	M.leprae rpoB gene
c	16	14	70.0	3474	23	AAS51357	Enterococcus faeca
c	17	14	70.0	3624	23	AAS52892	Enterococcus faeca
	18	14	70.0	6275	24	ABL32551	Human immune syste
	19	14	70.0	6319	23	ABL18447	Drosophila melanog
	20	14	70.0	9179	20	AAX13246	Enterococcus faeca
	21	14	70.0	9728	24	ABL33903	Human immune syste
	22	14	70.0	29555	23	ABL18446	Drosophila melanog
	23	13	65.0	58	22	AAF61643	Lactobacillus case
	24	13	65.0	234	17	AAT13651	AcNPV ORF 43, resi
	25	13	65.0	351	22	AAF61568	Lactobacillus case
	26	13	65.0	383	19	AAV04618	Flea aminopeptidas
	27	13	65.0	383	22	AAC90900	Flea aminopeptidas
c	28	13	65.0	421	23	AAS94185	DNA encoding novel
	29	13	65.0	537	19	AAV04619	Flea aminopeptidas
	30	13	65.0	537	22	AAC90901	Flea aminopeptidas
	31	13	65.0	667	22	AAF71326	Corynebacterium gl
c	32	13	65.0	1086	22	AAF27618	Mevalonate pathway
c	33	13	65.0	1227	23	AAS87269	DNA encoding novel
	34	13	65.0	1242	23	ABL22843	Drosophila melanog
c	35	13	65.0	1261	18	AAV74720	Staphylococcus aur
	36	13	65.0	1326	22	AAH68314	C glutamicum codin
c	37	13	65.0	1407	22	AAH53127	S. epidermidis ope
c	38	13	65.0	1473	21	AAC48699	Arabidopsis thalia
c	39	13	65.0	1475	21	AAC32775	Arabidopsis thalia
	40	13	65.0	1938	22	AAF89013	Murine FATP1 codin
	41	13	65.0	2109	23	AAS92952	DNA encoding novel
c	42	13	65.0	2192	23	AAS92789	DNA encoding novel
	43	13	65.0	2222	20	AAZ38124	Human FATP variant
	44	13	65.0	2470	23	AAS94186	DNA encoding novel
c	45	13	65.0	2870	23	ABL26802	Drosophila melanog

ALIGNMENTS

RESULT 1
AAA49824
ID AAA49824 standard; DNA; 20 BP.
XX
AC AAA49824;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene amplification primer rpoB-R.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX

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                     SIFAAIGVVSGTQLDPCQSPRPVSVIHIHGTADPLVRYHGGPGAGFARIDGPPVPDLN
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gene                 11859. .13487
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CDS                  11859. .13487
                     /gene="MT0701"
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                     /product="acyl-CoA dehydrogenase, putative"
                     /protein_id="AAK44926.1"
                     /db_xref="GI:13880223"
                     /translation="MSDTHVVTNQVPPLENYNPASSPVLIEALIQEGGQWGLDEVNEV
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                     IFLVLAQAPDGLSCFLLPRVLPDGTRNRMFLQRLKDKLGNHANASSEVEYDGAVAWLV
                     GEEGRGVPTIIEMVNLTRLDCALGSATSMRTGLTRAVHHAQHRKAFGAYLIDQPLMRN
                     VLADLAVEAEAATIVAMRMAGATDNAVRGNETEALLRRIGLAAAKYWVCKRSTAHAAE
                     ALECLGGNGYVEDSGMPRLYREAPLMGIWEGSGNVSALDTLRAMATRPACVEVLFDEL
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gene                 13498. .14436
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CDS                  13498. .14436
                     /gene="MT0702"
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                     /db_xref="GI:13880224"
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                     PEGHAFVADAVEHGFRDAVRRRDEPFGDYGRQASRV"
gene                 14439. .15161
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CDS                  14439. .15161
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Qy       1 tacggcgtttcgatgaaccc 20
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Search completed: August  7, 2002, 23:49:04
Job time: 9218 sec
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BASE COUNT      969 a   1534 c   1691 g    890 t
ORIGIN


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Qy      1 tacggcgtttcgatgaaccc 20
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Db   2611 TACGGCGTTTCGATGAACCC 2592


RESULT 15
AE006964/c
LOCUS       AE006964               19352 bp    DNA     linear   BCT 27-APR-2001
DEFINITION  Mycobacterium tuberculosis CDC1551,  section 50 of 280 of the
            complete genome.
ACCESSION   AE006964 AE000516
VERSION     AE006964.1  GI:13880217
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis CDC1551.
  ORGANISM  Mycobacterium tuberculosis CDC1551
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 19352)
  AUTHORS   Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O.,
            Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E.,
            Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M.,
            Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H.,
            Gill,J., Mikula,A. and Bishai,W.
  TITLE     Whole genome comparison of Mycobacterium tuberculosis clinical and
            laboratory strains
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 19352)
  AUTHORS   Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O.,
            Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E.,
            Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M.,
            Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H.,
            Gill,J., Mikula,A. and Bishai,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-2001) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .19352
                     /organism="Mycobacterium tuberculosis CDC1551"
                     /strain="CDC1551"
                     /db_xref="taxon:83331"
                     /note="clinical strain"
     gene            163. .3699
                     /gene="MT0695"
     CDS             163. .3699
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                     /note="similar to GB:L27989 GB:L05910 GB:U12205 SP:P47766
                     PID:149992; identified by sequence similarity; putative"
                     /codon_start=1
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                     /product="DNA-directed RNA polymerase, beta subunit"
                     /protein_id="AAK44921.1"
                     /db_xref="GI:13880218"
                     /translation="MLEGCILADSRQSKTAASPSPSRPQSSSNNSVPGAPNRVSFAKL
                     REPLEVPGLLDVQTDSFEWLIGSPRWRESAAERGDVNPVGGLEEVLYELSPIEDFSGS
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                     TEKGTFIINGTERVVVSQLVRSPGVYFDETIDKSTDKTLHSVKVIPSRGAWLEFDVDK
                     RDTVGVRIDRKRRQPVTVLLKALGWTSEQIVERFGFSEIMRSTLEKDNTVGTDEALLD
                     IYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARVGRYKVNKKLGLHVGEPITSSTLT
                     EEDVVATIEYLVRLHEGQTTMTVPGGVEVPVETDDIDHFGNRRLRTVGELIQNQIRVG
                     MSRMERVVRERMTTQDVEAITPQTLINIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLT
                     HKRRLSALGPGGLSRERAGLEVRDVHPSHYGRMCPIETPEGPNIGLIGSLSVYARVNP
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                     LVGTGMELRAAIDAGDVVVAEESGVIEEVSADYITVMHDNGTRRTYRMRKFARSNHGT
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                     LVEEDVLTSIHIEEHEIDARDTKLGAEEITRDIPNISDEVLADLDERGIVRIGAEVRD
                     GDILVGKVTPKGETELTPEERLLRAIFGEKAREVRDTSLKVPHGESGKVIGIRVFSRE
                     DEDELPAGVNELVRVYVAQKRKISDGDKLAGRHGNKGVIGKILPVEDMPFLADGTPVD
                     IILNTHGVPRRMNIGQILETHLGWCAHSGWKVDAAKGVPDWAARLPDELLEAQPNAIV
                     STPVFDGAQEAELQGLLSCTLPNRDGDVLVDADGKAMLFDGRSGEPFPYPVTVGYMYI
                     MKLHHLVDDKIHARSTGPYSMITQQPLGGKAQFGGQRFGEMECWAMQAYGAAYTLQEL
                     LTIKSDDTVGRVKVYEAIVKGENIPEPGIPESFKVLLKELQSLCLNVEVLSSDGAAIE
                     LREGEDEDLERAAANLGINLSRNESASVEDLA"
     gene            3744. .7694
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                     similarity; putative"
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                     LFKPFVMKRLVDLNHAQNIKSAKRMVERQRPQVWDVLEEVIAEHPVLLNRAPTLHRLG
                     IQAFEPMLVEGKAIQLHPLVCEAFNADFDGDQMAVHLPLSAEAQAEARILMLSSNNIL
                     SPASGRPLAMPRLDMVTGLYYLTTEVPEDTGEYQPASGDHPETGVYSSPAEAIMAADR
                     GVLSVRAKIKVRLTQLRPPVEIEAELFGHSGWQPGDAWMAETTLGRVMFNELLPLGYP
                     FVNKQMHKKVQAAIINDLAERYPMIVVAQTVDKLKDAGFYWATRSGVTVSMADVLVPP
                     RKKEILDHYEERADKVEKQFQRGALNHDERNEALVEIWKEATDEVGQALREHYPDDNP
                     IITIVDSGATGNFTQTRTLAGMKGLVTNPKGEFIPRPVKSSFREGLTVLEYFINTHGA
                     RKGLADTALRTADSGYLTRRLVDVSQDVIVREHDCQTERGIVVELAERAPDGTLIRDP
                     YIETSAYARTLGTDAVDEAGNVIVERGQDLGDPEIDALLAAGITQVKVRSVLTCATST
                     GVCATCYGRSMATGKLVDIGEAVGIVAAQSIGEPGTQLTMRTFHQGGVGEDITGGLPR
                     VQELFEARVPRGKAPIADVTGRVRLEDGERFYKITIVPDDGGEEVVYDKISKRQRLRV
                     FKHEDGSERVLSDGDHVEVGQQLMEGSADPHEVLRVQGPREVQIHLVREVQEVYRAQG
                     VSIHDKHIEVIVRQMLRRVTIIDSGSTEFLPGSLIDRAEFEAENRRVVAEGGEPAAGR
                     PVLMGITKASLATDSWLSAASFQETTRVLTDAAINCRSDKLNGLKENVIIGKLIPAGT
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     gene            complement(8058. .9972)
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  Best Local Similarity   100.0%;  Pred. No. 0.057;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
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Db   1547 TACGGCGTTTCGATGAACCC 1528


RESULT 13
MTU12205/c
LOCUS       MTU12205                3853 bp    DNA     linear   BCT 02-MAR-2000
DEFINITION  Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
            gene, partial cds.
ACCESSION   U12205
VERSION     U12205.1  GI:515684
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 3853)
  AUTHORS   Imboden,P., Troller,R., Marchesi,F., Telenti,A., Bodmer,T.,
            Cole,S., Schopfer,K. and Burkart,T.
  TITLE     The rpoB gene of Mycobacterium tuberculosis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3853)
  AUTHORS   Imboden,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-1994) Paul Imboden, Institute for Medical
            Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
            3010, Switzerland
FEATURES             Location/Qualifiers
     source          1. .3853
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                     /strain="H37Rv"
                     /db_xref="taxon:1773"
     gene            576. .>3853
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                     IYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARVGRYKVNKKLGLHVGEPITSSTLT
                     EEDVVATIEYLVRLHEGQTTMTVPGGVEVPVETDDIDHFGNRRLRTVGELIQNQIRVG
                     MSRMERVVRERMTTQDVEAITPQTLINIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLT
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                     FGFIETPYRKVVDGVVSDGIVYLTADEEDRHVVAQANSPIDADGRFVEPRVLVRRKAG
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                     LVGTGMELRAAIDAATSSSQESGVIEEVSADYITVMHDNGTRRTYRMRKFARSNHGTC
                     ANQCPIVDAGDRVEAGQVIADGPCTDDGEMALGKNLLVAIMPWEGHNYEDAIILSNRL
                     VEEDVLTSIHIEEHEIDARDTKLGAEEITRDIPNISDEVLADLDERGIVRIGAEVRDG
                     DILVGKVTPKGETELTPEERLLRAIFGEKAREVRDTSLKVPHGESGKVIGIRVFSRED
                     EDELPAGVNELVRVYVAQKRKISDGDKLAGRHGNKGVIGKILPVEDMPFLADGTPVDI
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BASE COUNT      723 a   1173 c   1293 g    664 t
ORIGIN
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Qy      1 tacggcgtttcgatgaaccc 20
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Db   2122 TACGGCGTTTCGATGAACCC 2103


RESULT 14
MSGRPOB/c
LOCUS       MSGRPOB                 5084 bp    DNA     linear   BCT 13-SEP-1994
DEFINITION  Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB)
            gene, complete cds and RNA polymerase beta'-subunit rpoC gene,
            partial cds.
ACCESSION   L27989
VERSION     L27989.1  GI:468333
KEYWORDS    RNA polymerase beta-subunit; rpoB gene.
SOURCE      Mycobacterium tuberculosis (strain Rv) DNA.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 5084)
  AUTHORS   Miller,L.P., Crawford,J.T. and Shinnick,T.M.
  TITLE     The rpoB gene of Mycobacterium tuberculosis
  JOURNAL   Antimicrob. Agents Chemother. 38 (4), 805-811 (1994)
  MEDLINE   94304130
FEATURES             Location/Qualifiers
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                     IYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARVGRYKVNKKLGLHVGEPITSSTLT
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                     MSRMERVVRERMTTQDVEAITPQTLINIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLT
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                     KLHHLVDDKIHARSTGPYSMITQQPLGGKAQFGGQRFGEMECWAMQAYGAAYTLQELL
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ACCESSION   AF060353
VERSION     AF060353.1  GI:3133464
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 705)
  AUTHORS   Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
            Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
  TITLE     Simultaneous genotyping and species identification using
            hybridization pattern recognition analysis of generic mycobacterium
            DNA arrays
  JOURNAL   Genome Res. 8 (5), 435-448 (1998)
  MEDLINE   98248685
REFERENCE   2  (bases 1 to 705)
  AUTHORS   Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
            Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-APR-1998) Division of Infectious Disease, Affymetrix,
            3380 Central Expressway, Santa Clara, CA 95051, USA
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:1773"
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                     /gene="rpoB"
     CDS             <1. .>705
                     /gene="rpoB"
                     /codon_start=3
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                     EVEYVPSSEVDYMDVSPRQMVSVATAMIPFLEHDDANRALMGANMQRQAVPLVRSEAP
                     LVGTGMELRAAIDAAT"
BASE COUNT      117 a    227 c    250 g    111 t
ORIGIN
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  Query Match             100.0%;  Score 20;  DB 1;  Length 705;
  Best Local Similarity   100.0%;  Pred. No. 0.054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    331 TACGGCGTTTCGATGAACCC 312
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```
RESULT  10
AR149128/c
LOCUS       AR149128                706 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 24 from patent US 6228575.
ACCESSION   AR149128
VERSION     AR149128.1  GI:15113719
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 706)
  AUTHORS   Gingeras,T.R., Mack,D., Chee,M.S., Berno,A.J., Stryer,L.,
            Ghandour,G. and Wang,C.
  TITLE     Chip-based species identification and phenotypic characterization
            of microorganisms
  JOURNAL   Patent: US 6228575-A 24 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .706
                     /organism="unknown"
BASE COUNT      117 a    227 c    250 g    111 t      1 others
ORIGIN
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  Query Match             100.0%;  Score 20;  DB 6;  Length 706;
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Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    332 TACGGCGTTTCGATGAACCC 313
```

```
RESULT  11
I50706/c
LOCUS       I50706                  970 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1 from patent US 5643723.
ACCESSION   I50706
VERSION     I50706.1  GI:2472409
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 970)
  AUTHORS   Persing,D.H., Hunt,J.J., Young,K.K.Y., Felmlee,T.A., Roberts,G.D.
            and Whelan,A.Christian.
  TITLE     Detection of a genetic locus encoding resistance to rifampin in
            mycobacterial cultures and in clinical specimens
  JOURNAL   Patent: US 5643723-A 1 01-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .970
                     /organism="unknown"
BASE COUNT      182 a    302 c    330 g    156 t
ORIGIN
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Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    671 TACGGCGTTTCGATGAACCC 652
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RESULT  12
AX111339/c
LOCUS       AX111339                3534 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 2072 from Patent WO0123604.
ACCESSION   AX111339
VERSION     AX111339.1  GI:13927631
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 3534)
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 2072 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .3534
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BASE COUNT      679 a   1081 c   1188 g    586 t
ORIGIN
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          jannaschii FEN-1 endonucleases
  JOURNAL   Patent: US 5843669-A 136 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .620
                     /organism="unknown"
BASE COUNT      103 a    201 c    214 g    102 t
ORIGIN
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    296 TACGGCGTTTCGATGAACCC 277
```

```
RESULT   5
AR062058/c
LOCUS       AR062058                620 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 137 from patent US 5843669.
ACCESSION   AR062058
VERSION     AR062058.1  GI:5989749
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
  TITLE     Cleavage of nucleic acid acid using thermostable methoanococcus
            jannaschii FEN-1 endonucleases
  JOURNAL   Patent: US 5843669-A 137 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .620
                     /organism="unknown"
BASE COUNT      103 a    201 c    214 g    102 t
ORIGIN
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    296 TACGGCGTTTCGATGAACCC 277
```

```
RESULT   6
AR062059
LOCUS       AR062059                620 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 138 from patent US 5843669.
ACCESSION   AR062059
VERSION     AR062059.1  GI:5989750
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
  TITLE     Cleavage of nucleic acid acid using thermostable methoanococcus
            jannaschii FEN-1 endonucleases
  JOURNAL   Patent: US 5843669-A 138 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .620
                     /organism="unknown"
BASE COUNT      101 a    214 c    202 g    103 t
ORIGIN
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  Best Local Similarity  100.0%;  Pred. No. 0.054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    325 TACGGCGTTTCGATGAACCC 344
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```
RESULT   7
AR062060
LOCUS       AR062060                620 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 139 from patent US 5843669.
ACCESSION   AR062060
VERSION     AR062060.1  GI:5989751
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
  TITLE     Cleavage of nucleic acid acid using thermostable methoanococcus
            jannaschii FEN-1 endonucleases
  JOURNAL   Patent: US 5843669-A 139 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .620
                     /organism="unknown"
BASE COUNT      102 a    214 c    201 g    103 t
ORIGIN
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  Query Match           100.0%;  Score 20;  DB 6;  Length 620;
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Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    325 TACGGCGTTTCGATGAACCC 344
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```
RESULT   8
AR062061
LOCUS       AR062061                620 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 140 from patent US 5843669.
ACCESSION   AR062061
VERSION     AR062061.1  GI:5989752
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
  TITLE     Cleavage of nucleic acid acid using thermostable methoanococcus
            jannaschii FEN-1 endonucleases
  JOURNAL   Patent: US 5843669-A 140 01-DEC-1998;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT      102 a    214 c    201 g    103 t
ORIGIN
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  Query Match           100.0%;  Score 20;  DB 6;  Length 620;
  Best Local Similarity  100.0%;  Pred. No. 0.054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    325 TACGGCGTTTCGATGAACCC 344
```

```
RESULT   9
AF060353/c
LOCUS       AF060353                705 bp    DNA     linear   BCT 15-MAY-1998
DEFINITION  Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB) gene,
```

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                /db_xref="taxon:1773"
     CDS        <1. .>432
                /codon_start=1
                /transl_table=11
                /product="RNA polymerase beta subunit"
                /protein_id="AAB59068.1"
                /db_xref="GI:149992"
                /translation="GNRRLRTVGELIQNQIRVGMSRMERVVRERMTTQDVEAITPQTL
                INIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDV
                HPSHYGRMCPIETPEGPNIGLIGSLSVYARVNPFGFIETPYR"
     variation  149
                /phenotype="rifampicin resistant in association with
                mutation 234 G"
                /replace="c"
     variation  188
                /phenotype="rifampicin resistant"
                /replace="c"
     variation  191
                /phenotype="rifampicin resistant in association with
                mutation 203 T"
                /replace="c"
     variation  194
                /phenotype="rifampicin resistant"
                /replace="t"
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                /replace="t"
     variation  208. .210
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                /replace=""
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                /replace="g"
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                /replace="g"
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                /replace="t"
     variation  254
                /phenotype="rifampicin resistant"
                /replace="c"
BASE COUNT       77 a    140 c    148 g     67 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.053;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    428 TACGGCGTTTCGATGAACCC 409


RESULT   2
AR067448/c
LOCUS       AR067448                 432 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 59 from patent US 5851763.
ACCESSION   AR067448
VERSION     AR067448.1  GI:5998670
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 432)
  AUTHORS   Heym,B., Cole,S., Young,D., Zhang,Y., Honore,N., Telenti,A. and
            Bodmer,T.
  TITLE     Rapid detection of antibiotic resistance in mycobacterium
            tuberculosis
  JOURNAL   Patent: US 5851763-A 59 22-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .432
                     /organism="unknown"
BASE COUNT       77 a    139 c    149 g     67 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 6;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 0.053;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    428 TACGGCGTTTCGATGAACCC 409


RESULT   3
AR062056/c
LOCUS       AR062056                 620 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 135 from patent US 5843669.
ACCESSION   AR062056
VERSION     AR062056.1  GI:5989747
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
  TITLE     Cleavage of nucleic acid acid using thermostable methoanococcus
            jannaschii FEN-1 endonucleases
  JOURNAL   Patent: US 5843669-A 135 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .620
                     /organism="unknown"
BASE COUNT      103 a    202 c    214 g    101 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    296 TACGGCGTTTCGATGAACCC 277


RESULT   4
AR062057/c
LOCUS       AR062057                 620 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 136 from patent US 5843669.
ACCESSION   AR062057
VERSION     AR062057.1  GI:5989748
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
  TITLE     Cleavage of nucleic acid acid using thermostable methoanococcus
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:49:03 ; Search time 2179.67 Seconds
(without alignments)
192.016 Million cell updates/sec

Title: US-09-786-105-4
Perfect score: 20
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
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28: em_un:*
29: em_vi:*
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32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	20	100.0	432	1	MSGRIFRNAP	L05910 Mycobacteri
c 2	20	100.0	432	6	AR067448	AR067448 Sequence
c 3	20	100.0	620	6	AR062056	AR062056 Sequence
c 4	20	100.0	620	6	AR062057	AR062057 Sequence
c 5	20	100.0	620	6	AR062058	AR062058 Sequence
6	20	100.0	620	6	AR062059	AR062059 Sequence
7	20	100.0	620	6	AR062060	AR062060 Sequence
8	20	100.0	620	6	AR062061	AR062061 Sequence
c 9	20	100.0	705	1	AF060353	AF060353 Mycobacte
c 10	20	100.0	706	6	AR149128	AR149128 Sequence
c 11	20	100.0	970	6	I50706	I50706 Sequence 1
c 12	20	100.0	3534	6	AX111339	AX111339 Sequence
c 13	20	100.0	3853	1	MTU12205	U12205 Mycobacteri
c 14	20	100.0	5084	1	MSGRPOB	L27989 Mycobacteri
c 15	20	100.0	19352	1	AE006964	AE006964 Mycobacte
c 16	20	100.0	19770	1	MTCI376	Z95972 Mycobacteri
c 17	17	85.0	3316	1	AF172323	AF172323 Bacillus
18	15	75.0	27	6	I50714	I50714 Sequence 9
c 19	15	75.0	11843	1	AE008100	AE008100 Agrobacte
c 20	15	75.0	13735	1	AE009134	AE009134 Agrobacte
21	15	75.0	239050	1	AL596169	AL596169 Listeria
22	14	70.0	143	3	AF277396	AF277396 Crithidia
23	14	70.0	409	1	CSPAG22R	Z47191 Calothrix D
24	14	70.0	442	8	AF080428	AF080428 Agrocybe
25	14	70.0	458	8	AF080421	AF080421 Agrocybe
26	14	70.0	518	1	AF325874	AF325874 Staphyloc
27	14	70.0	762	1	SHFENTC	M63306 S.flexneri
28	14	70.0	791	33	AC048639	Ac048639 Giardia i
29	14	70.0	1128	8	AB044172	AB044172 Yamagishi
c 30	14	70.0	1194	3	FHEFHMDA	L36247 Fasciola he
31	14	70.0	1959	8	ATHTUBA6A	M84699 Arabidopsis
c 32	14	70.0	2612	3	FHEFHMDB	L36248 Fasciola he
33	14	70.0	2615	10	RNPKCETA	X68400 R.norvegicu
34	14	70.0	3218	10	AF146518	AF146518 Rattus no
35	14	70.0	3240	8	SCU06465	U06465 Saccharomyc
c 36	14	70.0	3447	6	AR067447	AR067447 Sequence
37	14	70.0	3639	10	AF214568	AF214568 Rattus no
38	14	70.0	4075	10	AF146044	AF146044 Rattus no
39	14	70.0	4887	3	AY069181	AY069181 Drosophil
40	14	70.0	6211	3	CEF14A5	Z75951 Caenorhabdi
41	14	70.0	6275	6	AX345453	AX345453 Sequence
42	14	70.0	6275	6	AX348335	AX348335 Sequence
c 43	14	70.0	9086	1	AE001767	AE001767 Thermotog
44	14	70.0	9728	6	AX346805	AX346805 Sequence
45	14	70.0	9728	6	AX348479	AX348479 Sequence

ALIGNMENTS

RESULT 1
MSGRIFRNAP/c
LOCUS MSGRIFRNAP 432 bp DNA linear BCT 21-MAY-1993
DEFINITION Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin resistance gene, complete cds.
ACCESSION L05910
VERSION L05910.1 GI:149991
KEYWORDS RNA polymerase beta-subunit; rifampicin resistance.
SOURCE Mycobacterium tuberculosis (strain H37) DNA.
ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 432)
AUTHORS Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T., Colston,J., Matter,L., Schopfer,K. and Bodmer,T.
TITLE Detection of rifampicin-resistance mutation in Mycobacterium tuberculosis
JOURNAL Antimicrob. Agents Chemother. 341, 647-650 (1993)
FEATURES Location/Qualifiers
source 1. .432
/organism="Mycobacterium tuberculosis"
/strain="H37"

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  JOURNAL   Genome Res. 10 (12), 2030-2043 (2000)
  MEDLINE   20568492
COMMENT     On Aug 17, 1999 this sequence version replaced gi:5735350.
            Contact: Brian Oliver
            Laboratory of Cellular and Developmental Biology
            NIDDK, National Institutes of Health
            6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethesda, MD 20892 USA
            Fax: (301) 496 5239
            Email: oliver@helix.nih.gov,
            http://www.niddk.nih.gov/intram/people/boliver.htm
            Tissue isolation and library construction performed at the National
            Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
            http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
            and analyses performed by National Institutes of Health Intramural
            Sequencing Center (NISC; see http://www.nisc.nih.gov).
            Plate: 07  row: c  column: 12
            Seq primer: M13RP1 reverse primer (ABI).
FEATURES             Location/Qualifiers
     source          1. .379
                     /organism="Drosophila melanogaster"
                     /strain="y[*] w[67c1]/Y"
                     /db_xref="taxon:7227"
                     /clone="bs07c12"
                     /clone_lib="Drosophila melanogaster adult testis library"
                     /sex="male"
                     /dev_stage="1-5 day adult"
                     /lab_host="SOLR (Stratagene)"
                     /note="Organ: testis; Vector: pBlueScript SK (Stratagene);
                     Site_1: EcoR I; Site_2: Xho I; Testes dissected from 1-5
                     day adult y[*] w[67c1]/Y males raised at 25oC.  RNA
                     isolated using Trizol (Life Technologies) and a single
                     round of Poly(A)+ selection using Oligotex (Qiagen).  cDNA
                     library constructed using Stratagene ZAP-cDNA syntesis
                     kit.  Oligo dT-primed, size fractionated ~1-6 kb, and
                     directionally cloned at EcoRI and XhoI in Uni-ZAP XR.
                     Following a single round of amplification pBlueScript SK
                     phagemids were mass excised.  A distribution channel for
                     clones is being sought, but not currently available.
                     Requests for clones cannot be honored."
BASE COUNT      104 a     96 c    113 g     66 t
ORIGIN


  Query Match            75.0%;  Score 15;  DB 9;  Length 379;
  Best Local Similarity  100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 acggtcggcgagctg 16
          |||||||||||||||
Db     39 ACGGTCGGCGAGCTG 53


Search completed: August  7, 2002, 23:12:33
Job time: 11072 sec
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```
RESULT 13
BE423869/c
LOCUS       BE423869                237 bp    mRNA    linear   EST 24-JUL-2000
DEFINITION  WHE0067_F05_K09ZS Wheat endosperm cDNA library Triticum aestivum
            cDNA clone WHE0067_F05_K09, mRNA sequence.
ACCESSION   BE423869
VERSION     BE423869.1  GI:9421712
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 237)
  AUTHORS   Altenbach,S., Anderson,O.D., Chao,S., Galili,G., Han,P.S., Hsia
            ,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and
            Tong,J.C.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Endosperm cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES             Location/Qualifiers
     source          1. .237
                     /organism="Triticum aestivum"
                     /cultivar="Cheyenne"
                     /db_xref="taxon:4565"
                     /clone="WHE0067_F05_K09"
                     /clone_lib="Wheat endosperm cDNA library"
                     /tissue_type="Endosperm"
                     /dev_stage="5 to 30 days post anthesis seed"
                     /lab_host="E. coli SOLR"
                     /note="Vector: Lambda ZAP II, excised phagemid; Site_1:
                     EcoRI; Seeds collected, endosperm isolated, and RNA
                     prepared by Susan  Altenbach. Library constructed by
                     Stratagene, Inc. Plasmid DNA  preparations and DNA
                     sequencing were performed in the OD Anderson lab."
BASE COUNT       65 a     79 c     40 g     53 t
ORIGIN
```

```
  Query Match             75.0%;  Score 15;  DB 10;  Length 237;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 tcggcgagctgatcc 20
           ||||||||||||||||
Db      79 TCGGCGAGCTGATCC 65
```

```
RESULT 14
AI945868
LOCUS       AI945868                376 bp    mRNA    linear   EST 08-JAN-2001
DEFINITION  bs17g07.y1 Drosophila melanogaster adult testis library Drosophila
            melanogaster cDNA clone bs17g07 5', mRNA sequence.
ACCESSION   AI945868
VERSION     AI945868.2  GI:9991196
KEYWORDS    EST.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 376)
  AUTHORS   Andrews,J., Bouffard,G.G., Cheadle,C., Lu,J., Becker,K.G. and
            Oliver,B.
  TITLE     Gene discovery using computational and microarray analysis of
            transcription in the drosophila melanogaster testis
  JOURNAL   Genome Res. 10 (12), 2030-2043 (2000)
  MEDLINE   20568492
COMMENT     On Aug 17, 1999 this sequence version replaced gi:5736266.
            Contact: Brian Oliver
            Laboratory of Cellular and Developmental Biology
            NIDDK, National Institutes of Health
            6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethesda, MD 20892 USA
            Fax: (301) 496 5239
            Email: oliver@helix.nih.gov,
            http://www.niddk.nih.gov/intram/people/boliver.htm
            Tissue isolation and library construction performed at the National
            Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
            http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
            and analyses performed by National Institutes of Health Intramural
            Sequencing Center (NISC; see http://www.nisc.nih.gov).
            Plate: 17  row: g  column: 07
            Seq primer: M13RP1 reverse primer (ABI).
FEATURES             Location/Qualifiers
     source          1. .376
                     /organism="Drosophila melanogaster"
                     /strain="y[*] w[67c1]/Y"
                     /db_xref="taxon:7227"
                     /clone="bs17g07"
                     /clone_lib="Drosophila melanogaster adult testis library"
                     /sex="male"
                     /dev_stage="1-5 day adult"
                     /lab_host="SOLR (Stratagene)"
                     /note="Organ: testis; Vector: pBlueScript SK (Stratagene);
                     Site_1: EcoR I; Site_2: Xho I; Testes dissected from 1-5
                     day adult y[*] w[67c1]/Y males raised at 25oC.  RNA
                     isolated using Trizol (Life Technologies) and a single
                     round of Poly(A)+ selection using Oligotex (Qiagen).  cDNA
                     library constructed using Stratagene ZAP-cDNA syntesis
                     kit.  Oligo dT-primed, size fractionated -1-6 kb, and
                     directionally cloned at EcoRI and XhoI in Uni-ZAP XR.
                     Following a single round of amplification pBlueScript SK
                     phagemids were mass excised.  A distribution channel for
                     clones is being sought, but not currently available.
                     Requests for clones cannot be honored."
BASE COUNT      110 a     94 c    107 g     65 t
ORIGIN
```

```
  Query Match             75.0%;  Score 15;  DB 9;  Length 376;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 acggtcggcgagctg 16
           |||||||||||||||
Db     272 ACGGTCGGCGAGCTG 286
```

```
RESULT 15
AI944952
LOCUS       AI944952                379 bp    mRNA    linear   EST 08-JAN-2001
DEFINITION  bs07c12.y1 Drosophila melanogaster adult testis library Drosophila
            melanogaster cDNA clone bs07c12 5', mRNA sequence.
ACCESSION   AI944952
VERSION     AI944952.2  GI:9990300
KEYWORDS    EST.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 379)
  AUTHORS   Andrews,J., Bouffard,G.G., Cheadle,C., Lu,J., Becker,K.G. and
            Oliver,B.
  TITLE     Gene discovery using computational and microarray analysis of
            transcription in the drosophila melanogaster testis
```

```
FEATURES             Location/Qualifiers
     source          1. .606
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone="5333151"
                     /clone_lib="zebrafish adult brain"
                     /sex="mixed male and female"
                     /tissue_type="brain"
                     /dev_stage="adult"
                     /lab_host="E. coli DH10B"
                     /note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
                     Original library was constructed in lambdaZIPLOX.  Mass
                     excision of the cDNA library was performed to yield
                     pZIPLOX plasmids. Insert check was done in original
                     library."
BASE COUNT      209 a    133 c    139 g    125 t
ORIGIN


  Query Match             80.0%;  Score 16;  DB 10;  Length 606;
  Best Local Similarity   100.0%;  Pred. No. 74;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctg 16
          ||||||||||||||||
Db    452 TACGGTCGGCGAGCTG 437


RESULT  11
BI888442/c
LOCUS       BI888442                 640 bp    mRNA    linear   EST 12-OCT-2001
DEFINITION  ZF637-2-000197 Zebrafish shield stage whole embryo cDNA library
            MPMGp637 Danio rerio cDNA clone MPMGp637_18E17;MPMGp637E1718 5',
            mRNA sequence.
ACCESSION   BI888442
VERSION     BI888442.1  GI:16095713
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 640)
  AUTHORS   Clark,M., Aanstad,P., Hennig,S., Johnson,S.L. and Lehrach,H.
  TITLE     EST sequencing of a zebrafish shield stage cDNA library normalised
            by oligonucleotide fingerprinting
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Hennig S
            laboraty 123, dept.Lehrach
            Max-Planck-Institut fuer Molekulare Genetik
            Ihnestr.63-73, D-14195 Berlin, Germany
            Tel: +49 30 8413 1612
            Fax: +49 30 8413 1380
            Email: hennig@molgen.mpg.de
            5' EST sequencing of clones from a zebrafish shield stage library,
            normalised from 55,000 starting clones by oligonucleotide
            fingerprinting
            High quality sequence stop: 640.
FEATURES             Location/Qualifiers
     source          1. .640
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone="MPMGp637_18E17;MPMGp637E1718"
                     /clone_lib="Zebrafish shield stage whole embryo cDNA
                     library MPMGp637"
                     /tissue_type="whole embryo"
                     /dev_stage="shield stage, 6 hrs post-fertilisation"
                     /lab_host="E.coli, XL1 blue MRF"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI;
                     oligo-dT-NotI primed, SalI adaptors, directionally cloned,
                     library normalised by oligonucleotide fingerprinting"
BASE COUNT      209 a    152 c    139 g    139 t      1 others
ORIGIN


  Query Match             80.0%;  Score 16;  DB 10;  Length 640;
  Best Local Similarity   100.0%;  Pred. No. 74;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctg 16
          ||||||||||||||||
Db    541 TACGGTCGGCGAGCTG 526


RESULT  12
BE585978
LOCUS       BE585978                 708 bp    mRNA    linear   EST 17-AUG-2000
DEFINITION  Est#7pT7_A09_a9_065 KSU wheat Fusarium graminearum infected spike
            cDNA library Triticum aestivum cDNA clone Est#7pT7_A09_a9_065, mRNA
            sequence.
ACCESSION   BE585978
VERSION     BE585978.1  GI:9839010
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 708)
  AUTHORS   Fellers,J.P., Li,W.L., Hill-Ambroz,K., Matthews,A. and Gill,B.S.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Kansas State Unversity. Fusarium graminearum infected
            spike cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: John Fellers
            US Department of Agriculture, Agriculture Research Service, Plant
            Science and Entomology Unit
            Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State
            University, Manhattan, KS 66506, USA
            Tel: 785-532-2367
            Fax: 785-532-6167
            Email: jpf@alfalfa.ksu.edu
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .708
                     /organism="Triticum aestivum"
                     /cultivar="Sumai3"
                     /db_xref="taxon:4565"
                     /clone="Est#7pT7_A09_a9_065"
                     /clone_lib="KSU wheat Fusarium graminearum infected spike
                     cDNA library"
                     /tissue_type="Spike"
                     /dev_stage="Adult plant"
                     /lab_host="E. coli JM109"
                     /note="Vector: pGEM-T easy; Site_1: SacII; Site_2: SpeI;
                     Plants were grown in the greenhouse. Spikes were sprayed
                     with  Fusarium graminearum (at what stage). Total RNA, and
                     poly(A) RNA  were prepared from infected spikes. cDNA was
                     prepared using the  SmartTM PCR cDNA synthesis kit from
                     Clonetech. cDNA was cloned  into the pGEM-T easy vector
                     from Promega."
BASE COUNT      154 a    221 c    177 g    156 t
ORIGIN


  Query Match             80.0%;  Score 16;  DB 10;  Length 708;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 gtcggcgagctgatcc 20
          ||||||||||||||||
Db    559 GTCGGCGAGCTGATCC 574
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                    Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT       26 a     41 c     44 g     18 t      1 others
ORIGIN


  Query Match             80.0%;  Score 16;  DB 10;  Length 130;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 gtcggcgagctgatcc 20
           ||||||||||||||||
Db      90 GTCGGCGAGCTGATCC 75


RESULT   8
BM396091/c
LOCUS       BM396091                 132 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-17-B01.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM396091
VERSION     BM396091.1  GI:18196144
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila.
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1  (bases 1 to 132)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
            ,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .132
                     /organism="Tetrahymena thermophila"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT       27 a     42 c     44 g     19 t
ORIGIN


  Query Match             80.0%;  Score 16;  DB 10;  Length 132;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 gtcggcgagctgatcc 20
           ||||||||||||||||
Db      92 GTCGGCGAGCTGATCC 77


RESULT   9
BM398255/c
LOCUS       BM398255                 134 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-42-H08.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM398255
VERSION     BM398255.1  GI:18198308
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila.
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1  (bases 1 to 134)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
            ,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .134
                     /organism="Tetrahymena thermophila"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT       26 a     44 c     46 g     18 t
ORIGIN


  Query Match             80.0%;  Score 16;  DB 10;  Length 134;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 gtcggcgagctgatcc 20
           ||||||||||||||||
Db      94 GTCGGCGAGCTGATCC 79


RESULT  10
BI981973/c
LOCUS       BI981973                 606 bp    mRNA    linear   EST 24-OCT-2001
DEFINITION  fu53f08.y1 zebrafish adult brain Danio rerio cDNA clone 5333151 5'
            similar to TR:Q9Y4D4 Q9Y4D4 KIAA0648 PROTEIN ;, mRNA sequence.
ACCESSION   BI981973
VERSION     BI981973.1  GI:16371108
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 606)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
            ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
            ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
            Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
            Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
            and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Other_ESTs: fu53f08.x1
            Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
            Matthew Clark. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
            www.rzpd.de)
            High quality sequence stop: 446.
```

/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. The cDNA clones were in vivo excised to give pBluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech Univeristy. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 144 a 209 c 165 g 140 t
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 658;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ggtcggcgagctgatcc 20
||||||||||||||||||
Db 512 GGTCGGCGAGCTGATCC 528

RESULT 6
BG299722
LOCUS BG299722 828 bp mRNA linear EST 17-OCT-2001
DEFINITION HVSMEa0021I20f Hordeum vulgare seedling shoot EST library HVcDNA0001 (Cold stress) Hordeum vulgare cDNA clone HVSMEa0021I20f, mRNA sequence.
ACCESSION BG299722
VERSION BG299722.1 GI:13087434
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 828)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R., Choi,D.W., Fenton,R.D. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex cold-stressed seedling shoot cDNA library
JOURNAL Unpublished (2001)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 574
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 643.
FEATURES Location/Qualifiers
source 1. .828
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEa0021I20f"
/clone_lib="Hordeum vulgare seedling shoot EST library HVcDNA0001 (Cold stress)"
/tissue_type="Seedling shoot"
/lab_host="TJC121"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedlings were incubated at 5oC for 2 days. Shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 600000 pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 172 a 271 c 220 g 165 t
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 828;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ggtcggcgagctgatcc 20
||||||||||||||||||
Db 500 GGTCGGCGAGCTGATCC 516

RESULT 7
BM397871/c
LOCUS BM397871 130 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-38-C10.t.1 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM397871
VERSION BM397871.1 GI:18197924
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 130)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .130
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001)

surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. The cDNA clones were in vivo excised to give pBluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech Univeristy. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 122 a 180 c 134 g 122 t
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 558;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ggtcggcgagctgatcc 20
||||||||||||||||||
Db 514 GGTCGGCGAGCTGATCC 530

RESULT 4
BE195103
LOCUS BE195103 610 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEh0088E21f Hordeum vulgare 5-45 DAP spike EST library HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0088E21f, mRNA sequence.
ACCESSION BE195103
VERSION BE195103.3 GI:16321083
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 610)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton ,R.D., Close,S.J., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex 5-45 DAP spike cDNA library
JOURNAL Unpublished (2001)
COMMENT On Jun 26, 2000 this sequence version replaced gi:13187931.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 238
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 563.
FEATURES Location/Qualifiers
source 1. .610
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEh0088E21f"
/clone_lib="Hordeum vulgare 5-45 DAP spike EST library HVcDNA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Plants were grown in the greenhouse at the University of California, Riverside (Fenton, SJ Close, TJ Close). Whole spikes with awns trimmed were collected at 5, 10, 15, 20, 30 and 45 DAP (Fenton). Total RNA was prepared from each pool, equal quantities of all six RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi)in the TJ Close lab at the University of California, Riverside. Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 127 a 203 c 158 g 120 t 2 others
ORIGIN

Query Match 85.0%; Score 17; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ggtcggcgagctgatcc 20
||||||||||||||||||
Db 499 GGTCGGCGAGCTGATCC 515

RESULT 5
BE442518
LOCUS BE442518 658 bp mRNA linear EST 25-JUL-2000
DEFINITION WHE1101_H10_O19ZS Wheat etiolated seedling root normalized cDNA library Triticum aestivum cDNA clone WHE1101_H10_O19, mRNA sequence.
ACCESSION BE442518
VERSION BE442518.1 GI:9442034
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 658)
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
TITLE The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
FEATURES Location/Qualifiers
source 1. .658
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1101_H10_O19"
/clone_lib="Wheat etiolated seedling root normalized cDNA library"

/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. The cDNA clones were in vivo excised to give pBluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech Univeristy. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 84 a 130 c 124 g 84 t
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 422;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ggtcggcgagctgatcc 20
||||||||||||||||||
Db 86 GGTCGGCGAGCTGATCC 102

RESULT 2
BE445100
LOCUS BE445100 544 bp mRNA linear EST 25-JUL-2000
DEFINITION WHE1132_H08_P16ZS Wheat etiolated seedling root normalized cDNA library Triticum aestivum cDNA clone WHE1132_H08_P16, mRNA sequence.
ACCESSION BE445100
VERSION BE445100.1 GI:9444655
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 544)
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
TITLE The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
FEATURES Location/Qualifiers
source 1. .544
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1132_H08_P16"
/clone_lib="Wheat etiolated seedling root normalized cDNA library"
/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. The cDNA clones were in vivo excised to give pBluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech Univeristy. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 121 a 173 c 132 g 118 t
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 544;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ggtcggcgagctgatcc 20
||||||||||||||||||
Db 512 GGTCGGCGAGCTGATCC 528

RESULT 3
BE444713
LOCUS BE444713 558 bp mRNA linear EST 25-JUL-2000
DEFINITION WHE1137_H03_O05ZS Wheat etiolated seedling root normalized cDNA library Triticum aestivum cDNA clone WHE1137_H03_O05, mRNA sequence.
ACCESSION BE444713
VERSION BE444713.1 GI:9444264
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 558)
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
TITLE The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
FEATURES Location/Qualifiers
source 1. .558
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1137_H03_O05"
/clone_lib="Wheat etiolated seedling root normalized cDNA library"
/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:12:33 ; Search time 4095.84 Seconds
(without alignments)
65.906 Million cell updates/sec

Title: US-09-786-105-3
Perfect score: 20
Sequence: 1 tacggtcggcgagctgatcc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	17	85.0	422	10	BE443802	BE443802 WHE1122_B
	2	17	85.0	544	10	BE445100	BE445100 WHE1132_H
	3	17	85.0	558	10	BE444713	BE444713 WHE1137_H
	4	17	85.0	610	9	BE195103	BE195103 HVSMEh008
	5	17	85.0	658	10	BE442518	BE442518 WHE1101_H
	6	17	85.0	828	10	BG299722	BG299722 HVSMEa002
c	7	16	80.0	130	10	BM397871	BM397871 5009-0-38
c	8	16	80.0	132	10	BM396091	BM396091 5009-0-17
c	9	16	80.0	134	10	BM398255	BM398255 5009-0-42
c	10	16	80.0	606	10	BI981973	BI981973 fu53f08.y
c	11	16	80.0	640	10	BI888442	BI888442 ZF637-2-0
	12	16	80.0	708	10	BE585978	BE585978 Est#7pT7_
c	13	15	75.0	237	10	BE423869	BE423869 WHE0067_F
	14	15	75.0	376	9	AI945868	AI945868 bs17g07.y
	15	15	75.0	379	9	AI944952	AI944952 bs07c12.y
c	16	15	75.0	556	12	BH229591	BH229591 1006153C0
	17	15	75.0	568	10	BI628597	BI628597 RH57079.5
	18	15	75.0	652	10	BF489438	BF489438 AT25558.5
	19	15	75.0	655	10	BF489430	BF489430 AT25548.5
	20	15	75.0	667	10	BF489536	BF489536 AT25583.5
	21	15	75.0	703	10	BF496035	BF496035 AT09742.5
	22	15	75.0	722	10	BF496005	BF496005 AT09708.5
	23	15	75.0	958	10	BE969326	BE969326 601649529
c	24	15	75.0	984	12	CNS01GJZ	AL143232 Anopheles
c	25	15	75.0	1000	10	BG416363	BG416363 HVSMEk001
c	26	15	75.0	1188	10	BM477266	BM477266 AGENCOURT
	27	14	70.0	159	10	BI727507	BI727507 1031093A0
	28	14	70.0	180	10	C61884	C61884 C61884 Yuji
	29	14	70.0	239	10	BF920601	BF920601 QV0-NT015
	30	14	70.0	251	12	AQ906217	AQ906217 GSSTc0226
c	31	14	70.0	252	10	W87730	W87730 zh65g09.s1
c	32	14	70.0	292	9	BB347857	BB347857 BB347857
	33	14	70.0	299	10	BI133481	BI133481 UI-M-BH3-
c	34	14	70.0	318	10	M79472	M79472 wEST00009 M
	35	14	70.0	328	9	AW922029	AW922029 EST353333
c	36	14	70.0	329	10	H57342	H57342 yr11c05.s1
	37	14	70.0	339	9	AJ281216	AJ281216 4A3A-ABC-
	38	14	70.0	344	10	BE415176	BE415176 MWL024.B0
c	39	14	70.0	349	9	AU110574	AU110574 AU110574
c	40	14	70.0	349	10	BG274757	BG274757 WHE2233_G
	41	14	70.0	352	10	T83696	T83696 yd65c08.r1
c	42	14	70.0	360	9	AV186178	AV186178 AV186178
c	43	14	70.0	360	9	AV191317	AV191317 AV191317
c	44	14	70.0	360	9	AV192208	AV192208 AV192208
c	45	14	70.0	360	9	AV197881	AV197881 AV197881

ALIGNMENTS

RESULT 1
BE443802
LOCUS BE443802 422 bp mRNA linear EST 25-JUL-2000
DEFINITION WHE1122_B06_C12ZS Wheat etiolated seedling root normalized cDNA library Triticum aestivum cDNA clone WHE1122_B06_C12, mRNA sequence.
ACCESSION BE443802
VERSION BE443802.1 GI:9443341
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 422)
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
TITLE The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
FEATURES Location/Qualifiers
source 1. .422
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1122_B06_C12"
/clone_lib="Wheat etiolated seedling root normalized cDNA library"
/tissue_type="Root"

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FT                   /*tag=  s
FT                   /note= "primer NMQRQ-1"
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FT                   /*tag=  t
FT                   /note= "primer NMQRQ-2"
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PN   WO9533074-A1.
XX
PD   07-DEC-1995.
XX
PF   26-MAY-1995;   95WO-US06790.
XX
PR   26-MAY-1994;   94US-0250030.
XX
PA   (HOFF ) HOFFMANN LA ROCHE INC.
PA   (MAYO-) MAYO FOUNDATION.
XX
PI   Felmlee TA,  Hunt JM,  Persing DH,  Roberts GD,  Whelen AC;
PI   Young KKY;
XX
DR   WPI; 1996-030581/03.
XX
PT   Detection of Mycobacterium tuberculosis - by amplifying sample DNA
PT   with a primer set that targets portions of the gene encoding rpoB.
XX
PS   Disclosure; Fig.3; 54pp; English.
XX
CC   This oligonucleotide DNA primer is specific for Mycobacterium
CC   tuberculosis, and may be used to amplify a sample DNA by targeting
CC   a portion of the gene encoding rpoB.  The 1st several bases comprise a
CC   nonhybridizing tail consisting of filler bases followed by
CC   a restriction site incorporated to facilitate cloning using the
CC   amplicon at a later date, if desired.  The remaining bases hybridize
CC   to bacterial rpoB DNA.  The method provides for the detection of M.
CC   tuberculosis and the concurrent determination of its drug
CC   susceptibility, particularly to rifamycin.  The method can provide
CC   often greater than 95% sensitivity and 100% specificity.  The
CC   biological sample is a fluid or tissue sample from a human.
XX
SQ   Sequence 970 BP; 182 A; 302 C; 330 G; 156 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 17;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 0.023;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggtcggcgagctgatcc 20
           ||||||||||||||||||||
Db     261 tacggtcggcgagctgatcc 280


RESULT  15
AAH51976
ID   AAH51976 standard; DNA; 3519 BP.
XX
AC   AAH51976;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Mycobacterium tuberculosis potential drug target gene SEQ ID 30.
XX
KW   Drug target; growth; organism viability; characterisation; ds.
XX
OS   Mycobacterium tuberculosis.
XX
PN   WO200135317-A1.
XX
PD   17-MAY-2001.
XX
PF   13-NOV-2000; 2000WO-US31152.
XX
PR   12-NOV-1999;   99US-0165086.
PR   12-NOV-1999;   99US-0165124.
PR   01-FEB-2000; 2000US-0179531.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Eisenberg D,  Rotstein SH,  Marcotte EM;
XX
DR   WPI; 2001-329193/34.
DR   P-PSDB; AAG81125.
XX
PT   Identifying nucleotide or polypeptide sequence for use as drug target,
PT   involves providing algorithm that analyzes a functional relationship
PT   between nucleotide or polypeptide sequences, and comparing the
PT   sequences  -
XX
PS   Disclosure; Page 68-69; 207pp; English.
XX
CC   This invention relates to a method for identifying a nucleotide or
CC   polypeptide sequence that may be a drug target, or essential for growth
CC   or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
CC   represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
CC   tuberculosis proteins which are potential drug targets. The DNA and
CC   protein sequences are used to illustrate the method of the invention. The
CC   method involves providing an unknown nucleotide or polypeptide sequences,
CC   and comparing it to a number of sequences along with at least one
CC   algorithm capable of analysing a functional relationship between
CC   nucleotide and polypeptide sequences. The method is useful for
CC   characterising the function of nucleic acids and polypeptides that may be
CC   useful as a target for a drug or essential for the growth or viability of
CC   an organism.
XX
SQ   Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 22;  Length 3519;
  Best Local Similarity   100.0%;  Pred. No. 0.021;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggtcggcgagctgatcc 20
           ||||||||||||||||||||
Db    1119 tacggtcggcgagctgatcc 1138


Search completed: August  8, 2002, 00:01:25
Job time: 7614 sec
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Db      18 tacggtcggcgagctgatcc 37


RESULT  13
AAA49863
ID   AAA49863 standard; DNA; 480 BP.
XX
AC   AAA49863;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Mycobacterium tuberculosis rpoB gene (rifampin resistance).
XX
KW   Antibiotic resistance; rpoB gene; rifampin resistance; ss.
XX
OS   Mycobacterium tuberculosis.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag=  a
FT                   /note= "primer of AAA49823"
FT   primer_bind     372..391
FT                   /*tag=  b
FT                   /note= "primer of AAA49824"
XX
PN   WO200036142-A1.
XX
PD   22-JUN-2000.
XX
PF   10-DEC-1999;   99WO-CA01177.
XX
PR   11-DEC-1998;   98US-0111794.
XX
PA   (VISI-) VISIBLE GENETICS INC.
XX
PI   Shipman R;
XX
DR   WPI; 2000-431611/37.
XX
PT   Method for the detection and characterization of Mycobacterium
PT   tuberculosis with antibiotic resistance in a sample -
XX
PS   Disclosure; Page 5; 43pp; English.
XX
CC   The present sequence is that of the Mycobacterium tuberculosis
CC   rpoB (rifampin resistance) gene (bp2161-2640).  Amplification and
CC   cycle sequencing primers (see AAA49823-62) are used for the detection
CC   and analysis of antibiotic resistance-associated mutations in
CC   defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC   (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC   (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC   (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC   These primers can be used in a method for the detection and
CC   characterization of M. tuberculosis present in a sputum sample.
CC   The method involves performing a sequencing procedure, with or
CC   without prior amplification, to detect the presence of M.
CC   tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC   and 23S genes for the presence of antibiotic-inducing mutations.
CC   If M. tuberculosis is detected, a second sequencing procedure is
CC   performed on the sample to evaluate additional genes for the
CC   presence of antibiotic resistance-inducing mutations.  Genotypic
CC   tests are rapid, sensitive and accurate providing information as to
CC   antibiotic treatment options.
XX
SQ   Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 21;  Length 480;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggtcggcgagctgatcc 20
```

```
                    ||||||||||||||||||||
Db      41 tacggtcggcgagctgatcc 60


RESULT  14
AAT09676
ID   AAT09676 standard; DNA; 970 BP.
XX
AC   AAT09676;
XX
DT   15-OCT-1996  (first entry)
XX
DE   Mycobacterium tuberculosis rpoB gene DNA sequence.
XX
KW   Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;
KW   polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.
XX
OS   Mycobacterium tuberculosis.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     10..27
FT                   /*tag=  a
FT                   /note= "primer FENLFF"
FT   primer_bind     226..243
FT                   /*tag=  b
FT                   /note= "primer DDIDHL"
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FT                   /*tag=  c
FT                   /note= "primer DDIDH"
FT   primer_bind     338..364
FT                   /*tag=  d
FT                   /note= "primer rpo95"
FT   primer_bind     348..373
FT                   /*tag=  e
FT                   /note= "primer rpo105"
FT   primer_bind     354..373
FT                   /*tag=  f
FT                   /note= "primer KY290"
FT   misc_feature    372..373
FT                   /*tag=  g
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    433..434
FT                   /*tag=  h
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    438
FT                   /*tag=  i
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    468..469
FT                   /*tag=  j
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    486
FT                   /*tag=  k
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    501
FT                   /*tag=  l
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    516
FT                   /*tag=  m
FT                   /note= "M. tuberculosis signature nucleotide"
FT   primer_bind     516..535
FT                   /*tag=  n
FT                   /note= "primer rpo273"
FT   misc_feature    525
FT                   /*tag=  o
FT                   /note= "M. tuberculosis signature nucleotide"
FT   primer_bind     525..541
FT                   /*tag=  p
FT                   /note= "primer KY292"
FT   primer_bind     536..562
FT                   /*tag=  q
FT                   /note= "primer rpo293"
FT   primer_bind     640..666
FT                   /*tag=  r
```

CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 11
AAS99531
ID AAS99531 standard; DNA; 306 BP.
XX
AC AAS99531;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #6.
XX
KW Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
OS Mycobacterium bovis.
XX
PN WO200192573-A1.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-KR00904.
XX
PR 30-MAY-2000; 2000KR-0029369.
XX
PA (BIOM-) BIOMEDLAB CO LTD.
XX
PI Kim H, Kim N, Yoon S, Kim J, Park M;
XX
DR WPI; 2002-075472/10.
XX
PT Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -
XX
PS Disclosure; Page 21; 74pp; English.
XX
CC The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 12
AAQ61457
ID AAQ61457 standard; DNA; 432 BP.
XX
AC AAQ61457;
XX
DT 17-MAY-1994 (first entry)
XX
DE M.tuberculosis rpoB gene fragment.
XX
KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KW mutant; ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9322454-A.
XX
PD 11-NOV-1993.
XX
PF 30-APR-1993; 93WO-EP01063.
XX
PR 17-SEP-1992; 92FR-0011098.
PR 30-APR-1992; 92US-0875940.
PR 14-AUG-1992; 92US-0929206.
PR 16-APR-1993; 93FR-0004545.
XX
PA (ASSI-) ASSISTANCE PUBLIQUE.
PA (INSP) INST PASTEUR.
PA (MEDI-) MEDICAL RES COUNCIL.
PA (UYBE-) UNIV BERNE.
PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
PI Young D, Zhang Y;
XX
DR WPI; 1993-368812/46.
DR P-PSDB; AAR51372.
XX
PT Rapid detection of antibiotic resistance in Mycobacteria - esp.
PT isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in katG, rpoB or rpsL genes
XX
PS Example 2; Fig 13; 97pp; English.
XX
CC PCR amplification was used to obtain rpoB genes from rifampicin-
CC resistant Mycobacterium leprae strains. A comparison with the
CC sequence of the rpoB gene from sensitive strains (AAQ51532) revealed
CC mutations in the region encoding amino acids 400-450. The corresp.
CC region was isolated from M.tuberculosis (AAQ61457). A common
CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
SQ Sequence 432 BP; 78 A; 139 C; 148 G; 67 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20

DR WPI; 2002-075472/10.
XX
PT Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -
XX
PS Disclosure; Page 21; 74pp; English.
XX
CC The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 9
AAS99527
ID AAS99527 standard; DNA; 306 BP.
XX
AC AAS99527;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #2.
XX
KW Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
OS Mycobacterium africanum.
XX
PN WO200192573-A1.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-KR00904.
XX
PR 30-MAY-2000; 2000KR-0029369.
XX
PA (BIOM-) BIOMEDLAB CO LTD.
XX
PI Kim H, Kim N, Yoon S, Kim J, Park M;
XX
DR WPI; 2002-075472/10.
XX
PT Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -
XX
PS Disclosure; Page 21; 74pp; English.
XX
CC The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 10
AAS99530
ID AAS99530 standard; DNA; 306 BP.
XX
AC AAS99530;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #5.
XX
KW Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
OS Mycobacterium bovis.
XX
PN WO200192573-A1.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-KR00904.
XX
PR 30-MAY-2000; 2000KR-0029369.
XX
PA (BIOM-) BIOMEDLAB CO LTD.
XX
PI Kim H, Kim N, Yoon S, Kim J, Park M;
XX
DR WPI; 2002-075472/10.
XX
PT Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -
XX
PS Disclosure; Page 21; 74pp; English.
XX
CC The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of

ID AAX27179 standard; DNA; 306 BP.
XX
AC AAX27179;
XX
DT 27-MAY-1999 (first entry)
XX
DE RpoB gene fragment.
XX
KW RpoB gene; mycobacteria; phylogenetic tree construction;
KW mycobacterial species identification; phylogenetic analysis; ss.
XX
OS Mycobacteria bovis.
XX
PN WO9905316-A1.
XX
PD 04-FEB-1999.
XX
PF 28-JUL-1998; 98KR-0000228.
XX
PR 28-JUL-1997; 97KR-0035501.
XX
PA (BION-) BIONEER CORP.
XX
PI Kim B, Kook Y;
XX
DR WPI; 1998-539367/46.
XX
PT New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the rpoB gene from mycobacterial
PT species, useful for detecting and identifying mycobacterial species
XX
PS Claim 8; Page 64; 91pp; English.
XX
CC This sequence represents a mycobacterial rpoB gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the rpoB gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterising these species. In addition to
CC phylogenetic analysis, the rpoB gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in M. tuberculosis.
XX
SQ Sequence 306 BP; 56 A; 96 C; 107 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 7
AAX27180
ID AAX27180 standard; DNA; 306 BP.
XX
AC AAX27180;
XX
DT 27-MAY-1999 (first entry)
XX
DE RpoB gene fragment.
XX
KW RpoB gene; mycobacteria; phylogenetic tree construction;
KW mycobacterial species identification; phylogenetic analysis; ss.
XX
OS Mycobacteria bovis.
XX
PN WO9905316-A1.
XX
PD 04-FEB-1999.
XX
PF 28-JUL-1998; 98KR-0000228.
XX
PR 28-JUL-1997; 97KR-0035501.
XX
PA (BION-) BIONEER CORP.
XX
PI Kim B, Kook Y;
XX
DR WPI; 1998-539367/46.
XX
PT New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the rpoB gene from mycobacterial
PT species, useful for detecting and identifying mycobacterial species
XX
PS Claim 9; Page 64; 91pp; English.
XX
CC This sequence represents a mycobacterial rpoB gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the rpoB gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterising these species. In addition to
CC phylogenetic analysis, the rpoB gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in M. tuberculosis.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 5 tacggtcggcgagctgatcc 24

RESULT 8
AAS99526
ID AAS99526 standard; DNA; 306 BP.
XX
AC AAS99526;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #1.
XX
KW Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200192573-A1.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-KR00904.
XX
PR 30-MAY-2000; 2000KR-0029369.
XX
PA (BIOM-) BIOMEDLAB CO LTD.
XX
PI Kim H, Kim N, Yoon S, Kim J, Park M;
XX

```
CC   These primers can be used in a method for the detection and
CC   characterization of M. tuberculosis present in a sputum sample.
CC   The method involves performing a sequencing procedure, with or
CC   without prior amplification, to detect the presence of M.
CC   tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC   and 23S genes for the presence of antibiotic-inducing mutations.
CC   If M. tuberculosis is detected, a second sequencing procedure is
CC   performed on the sample to evaluate additional genes for the
CC   presence of antibiotic resistance-inducing mutations.  Genotypic
CC   tests are rapid, sensitive and accurate providing information as to
CC   antibiotic treatment options.
XX
SQ   Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;


  Query Match            100.0%;  Score 20;  DB 21;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0.031;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      1 tacggtcggcgagctgatcc 20


RESULT   4
AAX27214
ID   AAX27214 standard; DNA; 306 BP.
XX
AC   AAX27214;
XX
DT   27-MAY-1999  (first entry)
XX
DE   RpoB gene fragment.
XX
KW   RpoB gene; mycobacteria; phylogenetic tree construction;
KW   mycobacterial species identification; phylogenetic analysis; ss.
XX
OS   Mycobacteria tuberculosis.
XX
PN   WO9905316-A1.
XX
PD   04-FEB-1999.
XX
PF   28-JUL-1998;   98KR-0000228.
XX
PR   28-JUL-1997;   97KR-0035501.
XX
PA   (BION-) BIONEER CORP.
XX
PI   Kim B,  Kook Y;
XX
DR   WPI; 1998-539367/46.
XX
PT   New pair of polymerase chain reaction (PCR) primers - for
PT   sequence-specific amplification of the rpoB gene from mycobacterial
PT   species, useful for detecting and identifying mycobacterial species
XX
PS   Claim 43; Page 75-76; 91pp; English.
XX
CC   This sequence represents a mycobacterial rpoB gene fragment, that is
CC   amplified using the PCR primers of the invention. The primers form a
CC   method of detecting and identifying mycobacterial species by constructing
CC   a phylogenetic tree for the species. The use of the primers for
CC   sequence-specific amplification of the rpoB gene (encoding the beta
CC   subunit of RNA polymerase) from mycobacterial species provides an
CC   efficient way of characterising these species. In addition to
CC   phylogenetic analysis, the rpoB gene can be used as an alternative to
CC   the 16S rRNA gene because it has four subunits, which are highly
CC   conserved throughout prokaryotes. The method is particularly useful for
CC   slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
CC   susceptibility can be simultaneously determined in M. tuberculosis.
XX
SQ   Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;


  Query Match            100.0%;  Score 20;  DB 19;  Length 306;
  Best Local Similarity  100.0%;  Pred. No. 0.025;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 tacggtcggcgagctgatcc 24


RESULT   5
AAX27175
ID   AAX27175 standard; DNA; 306 BP.
XX
AC   AAX27175;
XX
DT   27-MAY-1999  (first entry)
XX
DE   RpoB gene fragment.
XX
KW   RpoB gene; mycobacteria; phylogenetic tree construction;
KW   mycobacterial species identification; phylogenetic analysis; ss.
XX
OS   Mycobacteria africanum.
XX
PN   WO9905316-A1.
XX
PD   04-FEB-1999.
XX
PF   28-JUL-1998;   98KR-0000228.
XX
PR   28-JUL-1997;   97KR-0035501.
XX
PA   (BION-) BIONEER CORP.
XX
PI   Kim B,  Kook Y;
XX
DR   WPI; 1998-539367/46.
XX
PT   New pair of polymerase chain reaction (PCR) primers - for
PT   sequence-specific amplification of the rpoB gene from mycobacterial
PT   species, useful for detecting and identifying mycobacterial species
XX
PS   Claim 4; Page 62-63; 91pp; English.
XX
CC   This sequence represents a mycobacterial rpoB gene fragment, that is
CC   amplified using the PCR primers of the invention. The primers form a
CC   method of detecting and identifying mycobacterial species by constructing
CC   a phylogenetic tree for the species. The use of the primers for
CC   sequence-specific amplification of the rpoB gene (encoding the beta
CC   subunit of RNA polymerase) from mycobacterial species provides an
CC   efficient way of characterising these species. In addition to
CC   phylogenetic analysis, the rpoB gene can be used as an alternative to
CC   the 16S rRNA gene because it has four subunits, which are highly
CC   conserved throughout prokaryotes. The method is particularly useful for
CC   slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
CC   susceptibility can be simultaneously determined in M. tuberculosis.
XX
SQ   Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;


  Query Match            100.0%;  Score 20;  DB 19;  Length 306;
  Best Local Similarity  100.0%;  Pred. No. 0.025;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 tacggtcggcgagctgatcc 24


RESULT   6
AAX27179
```

PT Probes and primers for determn. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene
XX
PS Claim 22; Page 39; 69pp; English.
XX
CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT12091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrids formed and
CC inferring the ARS, and opt. the spp., from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampicin and/or rifabutin resistance in M. leprae
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determn.
CC of ARS and spp. identity.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 1 tacggtcggcgagctgatcc 20

RESULT 2
AAA49823
ID AAA49823 standard; DNA; 20 BP.
XX
AC AAA49823;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene amplification primer rpoB-F.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 4; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene amplification primer rpoB-F (bp
CC 2201-2220). It is used with the reverse primer given in AAA49824
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
||||||||||||||||||||
Db 1 tacggtcggcgagctgatcc 20

RESULT 3
AAA49825
ID AAA49825 standard; DNA; 20 BP.
XX
AC AAA49825;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-5s.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene sequencing primer rpoB-5s (bp
CC 2201-2220). It is used with the reverse primer given in AAA49826 and
CC with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 8, 2002, 00:01:22 ; Search time 562.71 Seconds
(without alignments)
61.023 Million cell updates/sec

Title: US-09-786-105-3
Perfect score: 20
Sequence: 1 tacggtcggcgagctgatcc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	17	AAT12092	M. tuberculosis rp
	2	20	100.0	20	21	AAA49823	Mycobacterium tube
	3	20	100.0	20	21	AAA49825	Mycobacterium tube
	4	20	100.0	306	19	AAX27214	RpoB gene fragment
	5	20	100.0	306	19	AAX27175	RpoB gene fragment
	6	20	100.0	306	19	AAX27179	RpoB gene fragment
	7	20	100.0	306	19	AAX27180	RpoB gene fragment
	8	20	100.0	306	24	AAS99526	Mycobacterium spec
	9	20	100.0	306	24	AAS99527	Mycobacterium spec
	10	20	100.0	306	24	AAS99530	Mycobacterium spec
	11	20	100.0	306	24	AAS99531	Mycobacterium spec
	12	20	100.0	432	14	AAQ61457	M.tuberculosis rpo
	13	20	100.0	480	21	AAA49863	Mycobacterium tube
	14	20	100.0	970	17	AAT09676	Mycobacterium tube
	15	20	100.0	3519	22	AAH51976	Mycobacterium tube
	16	20	100.0	3534	22	AAH02079	Mycobacterium tube
	17	20	100.0	3853	21	AAA74651	Mycobacterium tube
	18	20	100.0	3853	21	AAA89994	M. tuberculosis rp
	19	19	95.0	306	19	AAX27217	RpoB gene fragment
	20	19	95.0	306	24	AAS99551	Mycobacterium spec
	21	19	95.0	21500	23	AAS59633	Propionibacterium
	22	18	90.0	25	17	AAT12091	M. tuberculosis rp
c	23	18	90.0	87	22	AAC88922	Mycobacterium tube
	24	16	80.0	306	19	AAX27212	RpoB gene fragment
	25	16	80.0	306	19	AAX27218	RpoB gene fragment
	26	16	80.0	306	19	AAX27193	RpoB gene fragment
	27	16	80.0	306	19	AAX27196	RpoB gene fragment
	28	16	80.0	306	19	AAX27204	RpoB gene fragment
	29	16	80.0	306	19	AAX27177	RpoB gene fragment
	30	16	80.0	306	19	AAX27182	RpoB gene fragment
	31	16	80.0	306	19	AAX27183	RpoB gene fragment
	32	16	80.0	306	19	AAX27186	RpoB gene fragment
	33	16	80.0	306	24	AAS99539	Mycobacterium spec
	34	16	80.0	306	24	AAS99557	Mycobacterium spec
	35	16	80.0	306	24	AAS99560	Mycobacterium spec
	36	16	80.0	306	24	AAS99565	Mycobacterium spec
	37	16	80.0	306	24	AAS99568	Mycobacterium spec
	38	16	80.0	27426	23	AAS59541	Propionibacterium
	39	15	75.0	1092	22	AAS02316	B. subtilis DNA en
	40	15	75.0	2488	23	ABL14021	Drosophila melanog
	41	15	75.0	2772	23	AAS54170	Pseudomonas aerugi
c	42	15	75.0	4544	23	ABL14020	Drosophila melanog
	43	15	75.0	4403765	22	AAI99683	Mycobacterium tube
	44	15	75.0	4411529	22	AAI99682	Mycobacterium tube
	45	14	70.0	50	19	AAV31045	Expression vector

ALIGNMENTS

RESULT 1
AAT12092
ID AAT12092 standard; DNA; 20 BP.
XX
AC AAT12092;
XX
DT 10-JUL-1996 (first entry)
XX
DE M. tuberculosis rpoB gene fragment amplification primer P2.
XX
KW Antibiotic; resistance; spectrum; gene; mycobacterium;
KW determination; amplification; tuberculosis; rpoB; fragment;
KW primer; differential; hybridisation; pattern; rifampicin;
KW rifabutin; species identification; ss.
XX
OS Synthetic.
XX
PN WO9533851-A2.
XX
PD 14-DEC-1995.
XX
PF 09-JUN-1995; 95WO-EP02230.
XX
PR 09-JUN-1994; 94EP-0870093.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI De Beenhouwer H, Jannes G, Machtelinckx L, Portaels F;
PI Rossau R;
XX
DR WPI; 1996-040250/04.
XX

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  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 3534)
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 2072 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
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                     /strain="Rv"
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Db   1137 TACGGTCGGCGAGCTGATCC 1156
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RESULT  15
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LOCUS       MTU12205                3853 bp    DNA     linear   BCT 02-MAR-2000
DEFINITION  Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
            gene, partial cds.
ACCESSION   U12205
VERSION     U12205.1  GI:515684
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 3853)
  AUTHORS   Imboden,P., Troller,R., Marchesi,F., Telenti,A., Bodmer,T.,
            Cole,S., Schopfer,K. and Burkart,T.
  TITLE     The rpoB gene of Mycobacterium tuberculosis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3853)
  AUTHORS   Imboden,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-1994) Paul Imboden, Institute for Medical
            Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
            3010, Switzerland
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:1773"
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     CDS             576. .>3853
                     /gene="rpoB"
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                     /product="RNA-polymerase beta subunit"
                     /protein_id="AAA20242.2"
                     /db_xref="GI:7144499"
                     /translation="MLEGCILADSRQSKTAASPSPSRPQSSSNNSVPGAPNRVSFAKL
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                     RDTVGVRIDRKRRQPVTVLLKALGWTSEQIVERFGFSEIMRSTLEKDNTVGTDEALLD
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                     mutation 234 G"
                     /replace="c"
     variation       188
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     variation       191
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                     mutation 203 T"
                     /replace="c"
     variation       194
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Db     18 TACGGTCGGCGAGCTGATCC 37
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LOCUS       AR067448                 432 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 59 from patent US 5851763.
ACCESSION   AR067448
VERSION     AR067448.1  GI:5998670
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 432)
  AUTHORS   Heym,B., Cole,S., Young,D., Zhang,Y., Honore,N., Telenti,A. and
            Bodmer,T.
  TITLE     Rapid detection of antibiotic resistance in mycobacterium
            tuberculosis
  JOURNAL   Patent: US 5851763-A 59 22-DEC-1998;
FEATURES             Location/Qualifiers
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ORIGIN


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Db     18 TACGGTCGGCGAGCTGATCC 37


RESULT  13
I50706
LOCUS       I50706                   970 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1 from patent US 5643723.
ACCESSION   I50706
VERSION     I50706.1  GI:2472409
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 970)
  AUTHORS   Persing,D.H., Hunt,J.J., Young,K.K.Y., Felmlee,T.A., Roberts,G.D.
            and Whelan,A.Christian.
  TITLE     Detection of a genetic locus encoding resistance to rifampin in
            mycobacterial cultures and in clinical specimens
  JOURNAL   Patent: US 5643723-A 1 01-JUL-1997;
FEATURES             Location/Qualifiers
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Db    261 TACGGTCGGCGAGCTGATCC 280


RESULT  14
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LOCUS       AX111339                 3534 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 2072 from Patent WO0123604.
ACCESSION   AX111339
VERSION     AX111339.1  GI:13927631
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
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Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   7
AR157007
LOCUS       AR157007                306 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 6 from patent US 6242584.
ACCESSION   AR157007
VERSION     AR157007.1  GI:15125711
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kook,Y.-H. and Kim,B.-J.
  TITLE     Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
  JOURNAL   Patent: US 6242584-A 6 05-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .306
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Qy      1 tacggtcggcgagctgatcc 20
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Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   8
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LOCUS       AR157008                306 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 7 from patent US 6242584.
ACCESSION   AR157008
VERSION     AR157008.1  GI:15125712
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kook,Y. and Kim,B.
  TITLE     Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
  JOURNAL   Patent: US 6242584-A 7 05-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .306
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BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


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Qy      1 tacggtcggcgagctgatcc 20
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Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   9
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LOCUS       AR157042                306 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 41 from patent US 6242584.
ACCESSION   AR157042
VERSION     AR157042.1  GI:15125746
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kook,Y. and Kim,B.
  TITLE     Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
  JOURNAL   Patent: US 6242584-A 41 05-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .306
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BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT  10
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LOCUS       AR157051                306 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 50 from patent US 6242584.
ACCESSION   AR157051
VERSION     AR157051.1  GI:15125755
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kook,Y. and Kim,B.
  TITLE     Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
  JOURNAL   Patent: US 6242584-A 50 05-JUN-2001;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT       56 a     94 c    108 g     48 t
ORIGIN


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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
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Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT  11
MSGRIFRNAP
LOCUS       MSGRIFRNAP              432 bp    DNA     linear   BCT 21-MAY-1993
DEFINITION  Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin
            resistance gene, complete cds.
ACCESSION   L05910
VERSION     L05910.1  GI:149991
KEYWORDS    RNA polymerase beta-subunit; rifampicin resistance.
SOURCE      Mycobacterium tuberculosis (strain H37) DNA.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 432)
  AUTHORS   Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T.,
            Colston,J., Matter,L., Schopfer,K. and Bodmer,T.
  TITLE     Detection of rifampicin-resistance mutation in Mycobacterium
            tuberculosis
  JOURNAL   Antimicrob. Agents Chemother. 341, 647-650 (1993)
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Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   4
AF057453
LOCUS       AF057453                306 bp    DNA     linear   BCT 17-SEP-1999
DEFINITION  Mycobacterium bovis BCG RNA polymerase beta (rpoB) gene, partial
            cds.
ACCESSION   AF057453
VERSION     AF057453.1  GI:5902493
KEYWORDS    .
SOURCE      Mycobacterium bovis BCG.
  ORGANISM  Mycobacterium bovis BCG
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
  MEDLINE   99262756
   PUBMED   10325313
REFERENCE   2  (bases 1 to 306)
  AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
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                     /strain="Tokyo T172"
                     /db_xref="taxon:33892"
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     CDS             <1. .>306
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ORIGIN


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DEFINITION  Mycobacterium tuberculosis RNA polymerase beta (rpoB) gene, partial
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ACCESSION   AF057454
VERSION     AF057454.1  GI:5902495
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
  MEDLINE   99262756
   PUBMED   10325313
REFERENCE   2  (bases 1 to 306)
  AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
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                     /db_xref="ATCC:27294"
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BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


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LOCUS       AR157003                306 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6242584.
ACCESSION   AR157003
VERSION     AR157003.1  GI:15125707
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kook,Y. and Kim,B.
  TITLE     Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
  JOURNAL   Patent: US 6242584-A 2 05-JUN-2001;
FEATURES             Location/Qualifiers
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BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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          Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
            Korea
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BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      5 TACGGTCGGCGAGCTGATCC 24


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LOCUS       AF057451                306 bp    DNA     linear   BCT 17-SEP-1999
DEFINITION  Mycobacterium bovis RNA polymerase beta (rpoB) gene, partial cds.
ACCESSION   AF057451
VERSION     AF057451.1  GI:5902489
KEYWORDS    .
SOURCE      Mycobacterium bovis.
  ORGANISM  Mycobacterium bovis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
  MEDLINE   99262756
   PUBMED   10325313
REFERENCE   2  (bases 1 to 306)
  AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
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     CDS             <1. .>306
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BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
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Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   3
AF057452
LOCUS       AF057452                306 bp    DNA     linear   BCT 17-SEP-1999
DEFINITION  Mycobacterium bovis BCG strain French 1173P2 RNA polymerase beta
            (rpoB) gene, partial cds.
ACCESSION   AF057452
VERSION     AF057452.1  GI:5902491
KEYWORDS    .
SOURCE      Mycobacterium bovis BCG.
  ORGANISM  Mycobacterium bovis BCG
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
  MEDLINE   99262756
   PUBMED   10325313
REFERENCE   2  (bases 1 to 306)
  AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
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BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 4.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:49:03 ; Search time 2179.67 Seconds
(without alignments)
192.016 Million cell updates/sec

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Perfect score: 20
Sequence: 1 tacggtcggcgagctgatcc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	306	1	AF057450	AF057450 Mycobacte
2	20	100.0	306	1	AF057451	AF057451 Mycobacte
3	20	100.0	306	1	AF057452	AF057452 Mycobacte
4	20	100.0	306	1	AF057453	AF057453 Mycobacte
5	20	100.0	306	1	AF057454	AF057454 Mycobacte
6	20	100.0	306	6	AR157003	AR157003 Sequence
7	20	100.0	306	6	AR157007	AR157007 Sequence
8	20	100.0	306	6	AR157008	AR157008 Sequence
9	20	100.0	306	6	AR157042	AR157042 Sequence
10	20	100.0	306	6	AR157051	AR157051 Sequence
11	20	100.0	432	1	MSGRIFRNAP	L05910 Mycobacteri
12	20	100.0	432	6	AR067448	AR067448 Sequence
13	20	100.0	970	6	I50706	I50706 Sequence 1
14	20	100.0	3534	6	AX111339	AX111339 Sequence
15	20	100.0	3853	1	MTU12205	U12205 Mycobacteri
16	20	100.0	5084	1	MSGRPOB	L27989 Mycobacteri
17	20	100.0	19352	1	AE006964	AE006964 Mycobacte
18	20	100.0	19770	1	MTCI376	Z95972 Mycobacteri
19	19	95.0	306	1	AF057493	AF057493 Mycobacte
20	19	95.0	306	6	AR157045	AR157045 Sequence
21	18	90.0	25	6	A47816	A47816 Sequence 30
C 22	18	90.0	87	6	AX050338	AX050338 Sequence
23	17	85.0	17407	1	AE006976	AE006976 Mycobacte
24	17	85.0	68848	1	MTV043	AL022004 Mycobacte
25	16	80.0	306	1	AF057456	AF057456 Mycobacte
26	16	80.0	306	1	AF057459	AF057459 Mycobacte
27	16	80.0	306	1	AF057460	AF057460 Mycobacte
28	16	80.0	306	1	AF057463	AF057463 Mycobacte
29	16	80.0	306	1	AF057471	AF057471 Mycobacte
30	16	80.0	306	1	AF057473	AF057473 Mycobacte
31	16	80.0	306	1	AF057480	AF057480 Mycobacte
32	16	80.0	306	1	AF057489	AF057489 Mycobacte
33	16	80.0	306	1	AF057496	AF057496 Corynebac
34	16	80.0	306	1	AF173087	AF173087 Mycobacte
35	16	80.0	306	6	AR157005	AR157005 Sequence
36	16	80.0	306	6	AR157010	AR157010 Sequence
37	16	80.0	306	6	AR157011	AR157011 Sequence
38	16	80.0	306	6	AR157014	AR157014 Sequence
39	16	80.0	306	6	AR157021	AR157021 Sequence
40	16	80.0	306	6	AR157024	AR157024 Sequence
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ALIGNMENTS

RESULT 1
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LOCUS AF057450 306 bp DNA linear BCT 17-SEP-1999
DEFINITION Mycobacterium africanum RNA polymerase beta (rpoB) gene, partial cds.
ACCESSION AF057450
VERSION AF057450.1 GI:5902487
KEYWORDS .
SOURCE Mycobacterium africanum.
ORGANISM Mycobacterium africanum
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T., Kim,E.C., Cha,C.Y. and Kook,Y.H.
TITLE Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)
JOURNAL J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
MEDLINE 99262756
PUBMED 10325313
REFERENCE 2 (bases 1 to 306)
AUTHORS Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,

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Search completed: August  7, 2002, 23:49:03
Job time: 9217 sec
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CC   compared to the cleavage products of reference gene sequences. The
CC   method is used for detecting mutation in the human p53 gene; for
CC   identifying strains of microorganisms, especially bacteria selected
CC   from the the group of members of the genera Campylobacter,
CC   Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC   The method may also be used for the identification of viruses,
CC   especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC   (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC   region of the Mycobacterium tuberculosis rpoB gene, which, when
CC   mutated is associated with rifampin resistance. The 620 bp region
CC   amplified spans both the H451Y and S456L mutations. The amplified
CC   fragments are given in AAT29124 (Wild type) and AAT29125-26
CC   (mutant sequences).
XX
SQ   Sequence 620 BP; 103 A; 201 C; 214 G; 102 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 17;  Length 620;
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Db    296 TACGGCGTTTCGATGAACCC 277


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XX
AC   AAT09676;
XX
DT   15-OCT-1996  (first entry)
XX
DE   Mycobacterium tuberculosis rpoB gene DNA sequence.
XX
KW   Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;
KW   polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.
XX
OS   Mycobacterium tuberculosis.
XX
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FT                   /*tag= g
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    433..434
FT                   /*tag= h
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    438
FT                   /*tag= i
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    468..469
FT                   /*tag= j
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    486
FT                   /*tag= k
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    501
FT                   /*tag= l
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    516
FT                   /*tag= m
FT                   /note= "M. tuberculosis signature nucleotide"
FT   primer_bind     516..535
FT                   /*tag= n
FT                   /note= "primer rpo273"
FT   misc_feature    525
FT                   /*tag= o
FT                   /note= "M. tuberculosis signature nucleotide"
FT   primer_bind     525..541
FT                   /*tag= p
FT                   /note= "primer KY292"
FT   primer_bind     536..562
FT                   /*tag= q
FT                   /note= "primer rpo293"
FT   primer_bind     640..666
FT                   /*tag= r
FT                   /note= "primer rpo397"
FT   primer_bind     952..966
FT                   /*tag= s
FT                   /note= "primer NMQRQ-1"
FT   primer_bind     952..966
FT                   /*tag= t
FT                   /note= "primer NMQRQ-2"
XX
PN   WO9533074-A1.
XX
PD   07-DEC-1995.
XX
PF   26-MAY-1995;   95WO-US06790.
XX
PR   26-MAY-1994;   94US-0250030.
XX
PA   (HOFF ) HOFFMANN LA ROCHE INC.
PA   (MAYO-) MAYO FOUNDATION.
XX
PI   Felmlee TA,  Hunt JM,  Persing DH,  Roberts GD,  Whelen AC;
PI   Young KKY;
XX
DR   WPI; 1996-030581/03.
XX
PT   Detection of Mycobacterium tuberculosis - by amplifying sample DNA
PT   with a primer set that targets portions of the gene encoding rpoB.
XX
PS   Disclosure; Fig.3; 54pp; English.
XX
CC   This oligonucleotide DNA primer is specific for Mycobacterium
CC   tuberculosis, and may be used to amplify a sample DNA by targeting
CC   a portion of the gene encoding rpoB.  The 1st several bases comprise a
CC   nonhybridizing tail consisting of filler bases followed by
CC   a restriction site incorporated to facilitate cloning using the
CC   amplicon at a later date, if desired.  The remaining bases hybridize
CC   to bacterial rpoB DNA.  The method provides for the detection of M.
CC   tuberculosis and the concurrent determination of its drug
CC   susceptibility, particularly to rifamycin.  The method can provide
CC   often greater than 95% sensitivity and 100% specificity.  The
CC   biological sample is a fluid or tissue sample from a human.
XX
SQ   Sequence 970 BP; 182 A; 302 C; 330 G; 156 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 17;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 0.0071;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    671 TACGGCGTTTCGATGAACCC 652
```

```
RESULT   9
AAH51976/c
ID   AAH51976 standard; DNA; 3519 BP.
XX
AC   AAH51976;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Mycobacterium tuberculosis potential drug target gene SEQ ID 30.
XX
KW   Drug target; growth; organism viability; characterisation; ds.
XX
OS   Mycobacterium tuberculosis.
XX
PN   WO200135317-A1.
XX
PD   17-MAY-2001.
XX
PF   13-NOV-2000; 2000WO-US31152.
XX
PR   12-NOV-1999;   99US-0165086.
PR   12-NOV-1999;   99US-0165124.
PR   01-FEB-2000; 2000US-0179531.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Eisenberg D,  Rotstein SH,  Marcotte EM;
XX
DR   WPI; 2001-329193/34.
DR   P-PSDB; AAG81125.
XX
PT   Identifying nucleotide or polypeptide sequence for use as drug target,
PT   involves providing algorithm that analyzes a functional relationship
PT   between nucleotide or polypeptide sequences, and comparing the
PT   sequences  -
XX
PS   Disclosure; Page 68-69; 207pp; English.
XX
CC   This invention relates to a method for identifying a nucleotide or
CC   polypeptide sequence that may be a drug target, or essential for growth
CC   or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
CC   represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
CC   tuberculosis proteins which are potential drug targets. The DNA and
CC   protein sequences are used to illustrate the method of the invention. The
CC   method involves providing an unknown nucleotide or polypeptide sequences,
CC   and comparing it to a number of sequences along with at least one
CC   algorithm capable of analysing a functional relationship between
CC   nucleotide and polypeptide sequences. The method is useful for
CC   characterising the function of nucleic acids and polypeptides that may be
CC   useful as a target for a drug or essential for the growth or viability of
CC   an organism.
XX
SQ   Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 22;  Length 3519;
  Best Local Similarity   100.0%;  Pred. No. 0.0064;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db   1529 TACGGCGTTTCGATGAACCC 1510


RESULT  10
AAH02079/c
ID   AAH02079 standard; DNA; 3534 BP.
XX
AC   AAH02079;
XX
DT   24-JUL-2001  (first entry)
XX
DE   Mycobacterium tuberculosis nucleotide sequence SEQ ID NO:2072.
XX
KW   Species specific; genus specific; family specific; probe; detection;
KW   identification; algal; archaeal; bacterial; fungal; parasitical;
KW   microorganism; diagnosis; translation elongation factor Tu; toxin;
KW   translation elongation factor G; RecA recombinase; resistance;
KW   catalytic subunit of proton-translocating ATPase; antimicrobial;
KW   vaccine; primer; ds.
XX
OS   Mycobacterium tuberculosis.
XX
PN   WO200123604-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-CA01150.
XX
PR   28-SEP-1999;   99CA-2283458.
PR   19-MAY-2000; 2000CA-2307010.
XX
PA   (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI   Bergeron MG,  Boissinot M,  Huletsky A,  Menard C,  Ouellette M;
PI   Picard FJ,  Roy PH;
XX
DR   WPI; 2001-245006/25.
XX
PT   Nucleic acid sequences are used to generate universal probes and
PT   primers which can be used to identify and detect the presence of algal,
PT   archaeal, bacterial, fungal and parasitical species in a test sample -
XX
PS   Disclosure; Page 1478-1479; 1580pp; English.
XX
CC   The present invention describes a method for generating a repertory of
CC   nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC   and/or primers are derived. The method comprises amplifying the nucleic
CC   acids of determined algal, archaeal, bacterial, fungal and parasitical
CC   species with a combination of defined primer pairs. The method can be
CC   used for producing probes and/or primers for detecting one or more
CC   related microorganisms e.g. algae, archaea, bacteria, fungi and
CC   parasites, for universal detection and for specific and ubiquitous
CC   detection and identification of an algal, archaeal, bacterial, fungal
CC   and parasitical species, genus, family and group. A nucleic acid (I)
CC   obtained using the method of the invention can be used for the universal
CC   detection of any bacterium, fungus or parasite in a sample and for the
CC   detection of at least one antimicrobial agent resistance gene or at
CC   least one toxin gene. hexA nucleic acids are used for the specific and
CC   ubiquitous detection and for identification of Streptococcus pneumoniae.
CC   (I) can be used to design a therapeutic agent which is effective against
CC   microorganisms. Microbial species or genus or family or phylum or group
CC   which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC   Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC   Mycobacteriaceae family, Pseudomonads group, Streptococcus sp.,
CC   Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests
CC   provides faster results than substrate specificity tests as results can
CC   be determined in an hour and improved accuracy is also achieved.
CC   AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
CC   which are given in the exemplification of the present invention.
XX
SQ   Sequence 3534 BP; 679 A; 1081 C; 1188 G; 586 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 22;  Length 3534;
  Best Local Similarity   100.0%;  Pred. No. 0.0064;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db   1547 TACGGCGTTTCGATGAACCC 1528


RESULT  11
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```
AAA74651/c
ID   AAA74651 standard; DNA; 3853 BP.
XX
AC   AAA74651;
XX
DT   06-DEC-2000  (first entry)
XX
DE   Mycobacterium tuberculosis rpoB gene.
XX
KW   Mycobacterium tuberculosis; rpoB; RNA polymerase beta subunit;
KW   rifampin resistance; mutation detection; ds.
XX
OS   Mycobacterium tuberculosis.
XX
PN   WO200043546-A2.
XX
PD   27-JUL-2000.
XX
PF   20-DEC-1999;   99WO-US30377.
XX
PR   19-JAN-1999;   99US-0233996.
XX
PA   (DADE-) DADE BEHRING INC.
XX
PI   Liu YP,  Kurn N;
XX
DR   WPI; 2000-524243/47.
XX
PT   Method for detecting drug resistance in a strain of an organism,
PT   particularly for detecting rifampin resistance in Mycobacterium
PT   tuberculosis  -
XX
PS   Example 1; Fig 4; 86pp; English.
XX
CC   The present sequence is the rpoB gene from Mycobacterium tuberculosis.
CC   Rifampin resistance is largely associated with point mutations
CC   localised in a small core region of 81 base pairs in the rpoB gene, which
CC   encodes the RNA polymerase beta subunit. To detect a mutation, a complex
CC   is formed comprising a first sequence representing the predetermined
CC   region of the gene of the organism and a second sequence representing the
CC   corresponding region of the gene of the wild type organism in double
CC   stranded form. Each member of at least one pair of non-complementary
CC   strands within the complex has a label. The association of the labels in
CC   the complex is related to the presence of the mutation. The presence of
CC   the mutation is related to the drug resistance of the strain.
XX
SQ   Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 21;  Length 3853;
  Best Local Similarity   100.0%;  Pred. No. 0.0064;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db   2122 TACGGCGTTTCGATGAACCC 2103


RESULT  12
AAA89994/c
ID   AAA89994 standard; DNA; 3853 BP.
XX
AC   AAA89994;
XX
DT   18-DEC-2000  (first entry)
XX
DE   M. tuberculosis rpoB gene encoding RNA polymerase beta subunit.
XX
KW   Drug resistance; rifampin; rifampicin; pyrazinamide; rpoB;
KW   RNA polymerase beta subunit; ds.
XX
OS   Mycobacterium tuberculosis.
XX
PN   WO200043545-A2.
XX
PD   27-JUL-2000.
XX
PF   14-DEC-1999;   99WO-US29517.
XX
PR   19-JAN-1999;   99US-0233996.
PR   22-APR-1999;   99US-0296894.
XX
PA   (DADE-) DADE BEHRING INC.
XX
PI   Liu YP,  Kurn N;
XX
DR   WPI; 2000-499235/44.
XX
PT   Detecting resistance of drugs such as rifampicin in strains of
PT   Mycobacterium, comprising detecting mutations in a gene and relating
PT   them to drug resistance -
XX
PS   Example 1; Fig 4; 91pp; English.
XX
CC   This invention relates to a method for detecting drug resistance in a
CC   strain of an organism. The method comprises detecting the presence of at
CC   least 1 mutation in a first sequence and relating the presence of the
CC   mutation to drug resistance. Included in the invention are a kit for
CC   carrying out the method and a method for detecting the presence of a
CC   difference between two related nucleic acid sequences in an organism. The
CC   methods are useful for detecting resistance to drugs such rifampin and
CC   pyrazinamide in Mycobacterium. The present sequence represents the
CC   Mycobacterium tuberculosis rpoB gene (which encodes the RNA polymerase
CC   beta subunit). The sequence is used in an example of the method of the
CC   invention for the detection of rifampin resistance in M. tuberculosis.
XX
SQ   Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 21;  Length 3853;
  Best Local Similarity   100.0%;  Pred. No. 0.0064;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db   2122 TACGGCGTTTCGATGAACCC 2103


RESULT  13
AAT12096
ID   AAT12096 standard; DNA; 19 BP.
XX
AC   AAT12096;
XX
DT   10-JUL-1996  (first entry)
XX
DE   M. tuberculosis rpoB gene fragment amplification primer P6.
XX
KW   Antibiotic; resistance; spectrum; gene; mycobacterium;
KW   determination; amplification; tuberculosis; rpoB; fragment;
KW   primer; differential; hybridisation; pattern; rifampicin;
KW   rifabutin; species identification; ss.
XX
OS   Synthetic.
XX
PN   WO9533851-A2.
XX
PD   14-DEC-1995.
XX
PF   09-JUN-1995;   95WO-EP02230.
XX
PR   09-JUN-1994;   94EP-0870093.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   De Beenhouwer H,  Jannes G,  Machtelinckx L,  Portaels F;
```

```
PI   Rossau R;
XX
DR   WPI; 1996-040250/04.
XX
PT   Probes and primers for determn. of antibiotic resistance spectrum of
PT   Mycobacterium, opt. coupled with species identification - from
PT   different patterns of hybridisation with rpoB gene
XX
PS   Claim 22; Page 39; 69pp; English.
XX
CC   The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC   determined by amplifying the relevant part of the antibiotic
CC   resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC   amplified using the primer set AAT12091-98, hybridising it with at
CC   least 1 rpoB gene probe, detecting the hybrids formed and
CC   inferring the ARS, and opt. the spp., from the differential
CC   hybridisation patterns. The method is partic. useful for the
CC   detection of rifampicin and/or rifabutin resistance in M. leprae
CC   or M. tuberculosis, and mycobacterial spp. identification. The
CC   method is rapid and reliable and provides simultaneous determn.
CC   of ARS and spp. identity.
XX
SQ   Sequence 19 BP; 4 A; 5 C; 5 G; 5 T; 0 other;


  Query Match             95.0%;  Score 19;  DB 17;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0.038;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaacc 19
           ||||||||||||||||||||
Db       1 tacggcgtttcgatgaacc 19


RESULT  14
AAT09670
ID   AAT09670 standard; DNA; 27 BP.
XX
AC   AAT09670;
XX
DT   15-OCT-1996  (first entry)
XX
DE   Mycobacterium tuberculosis 27-mer oligonucleotide DNA primer rpo397.
XX
KW   Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;
KW   polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.
XX
OS   Synthetic.
XX
PN   WO9533074-A1.
XX
PD   07-DEC-1995.
XX
PF   26-MAY-1995;   95WO-US06790.
XX
PR   26-MAY-1994;   94US-0250030.
XX
PA   (HOFF ) HOFFMANN LA ROCHE INC.
PA   (MAYO-) MAYO FOUNDATION.
XX
PI   Felmlee TA,  Hunt JM,  Persing DH,  Roberts GD,  Whelen AC;
PI   Young KKY;
XX
DR   WPI; 1996-030581/03.
XX
PT   Detection of Mycobacterium tuberculosis - by amplifying sample DNA
PT   with a primer set that targets portions of the gene encoding rpoB.
XX
PS   Claim 9; Page 39; 54pp; English.
XX
CC   This oligonucleotide DNA primer is specific for Mycobacterium
CC   tuberculosis, and may be used to amplify a sample DNA by targeting
CC   a portion of the gene encoding rpoB.  The method provides for the
CC   detection of M. tuberculosis and the concurrent determination of its
CC   drug susceptibility, particularly to rifamycin.  The method can
CC   provide often greater than 95% sensitivity and 100% specificity.
CC   The biological sample is a fluid or tissue sample from a human.
XX
SQ   Sequence 27 BP; 6 A; 7 C; 8 G; 6 T; 0 other;


  Query Match             75.0%;  Score 15;  DB 17;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 8.8;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 cgtttcgatgaaccc 20
           |||||||||||||||
Db       1 cgtttcgatgaaccc 15


RESULT  15
AAQ51532/c
ID   AAQ51532 standard; DNA; 3447 BP.
XX
AC   AAQ51532;
XX
DT   17-MAY-1994  (first entry)
XX
DE   M.leprae rpoB gene.
XX
KW   rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KW   mutant; ss.
XX
OS   Mycobacterium leprae.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..3447
FT                   /*tag= a
FT                   /note= "rifampicin-sensitive; in resistant
FT                           strains the Ser codon (TCG at
FT                           nucleotides 1273-1275) is often mutated
FT                           to a Phe, Met or esp. Leu codon"
XX
PN   WO9322454-A.
XX
PD   11-NOV-1993.
XX
PF   30-APR-1993;   93WO-EP01063.
XX
PR   17-SEP-1992;   92FR-0011098.
PR   30-APR-1992;   92US-0875940.
PR   14-AUG-1992;   92US-0929206.
PR   16-APR-1993;   93FR-0004545.
XX
PA   (ASSI-) ASSISTANCE PUBLIQUE.
PA   (INSP ) INST PASTEUR.
PA   (MEDI-) MEDICAL RES COUNCIL.
PA   (UYBE-) UNIV BERNE.
PA   (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI   Bodmer T,  Cole S,  Heym B,  Honore N,  Telenti A;
PI   Young D,  Zhang Y;
XX
DR   WPI; 1993-368812/46.
DR   P-PSDB; AAR43671.
XX
PT   Rapid detection of antibiotic resistance in Mycobacteria - esp.
PT   isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT   by detecting mutation in katG, rpoB or rpsL genes
XX
PS   Example 2; Fig 12; 97pp; English.
XX
CC   PCR amplification was used to obtain rpoB genes from rifampicin-
CC   resistant Mycobacterium leprae strains. A comparison with the
CC   sequence of the rpoB gene from sensitive strains (AAQ51532) revealed
CC   mutations in the region encoding amino acids 400-450. A common
```

CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
SQ Sequence 3447 BP; 687 A; 965 C; 1139 G; 656 T; 0 other;

Query Match 70.0%; Score 14; DB 14; Length 3447;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       7 gtttcgatgaaccc 20
           ||||||||||||||
Db    1448 GTTTCGATGAACCC 1435
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Job time: 7615 sec

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OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:12:33 ; Search time 4095.84 Seconds
(without alignments)
65.906 Million cell updates/sec

Title: US-09-786-105-4
Perfect score: 20
Sequence: 1 tacggcgtttcgatgaaccc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	17	85.0	234	10	W06754	W06754 SMEST0390 S
c 2	17	85.0	579	10	T24127	T24127 SMEST0325 S
3	16	80.0	624	10	BE896357	BE896357 601439015
4	15	75.0	384	10	BM077908	BM077908 pb21g06.y
c 5	15	75.0	452	9	AW694629	AW694629 NF078E03S
6	15	75.0	517	12	TA247H04P	AL483262 T. brucei
7	15	75.0	536	12	AQ783856	AQ783856 HS_2001_A
8	15	75.0	537	12	TA140G03P	AL466454 T. brucei
c 9	15	75.0	540	12	TA190A10P	AL477985 T. brucei
10	15	75.0	631	12	BH615799	BH615799 BMBAC304F
11	15	75.0	690	9	BE053145	BE053145 GA__Ea000
c 12	15	75.0	1033	12	CNS040YP	AL269530 Tetraodon
13	15	75.0	1218	10	BM007170	BM007170 603614933
c 14	14	70.0	247	9	AV640031	AV640031 AV640031
c 15	14	70.0	269	9	AV640876	AV640876 AV640876
c 16	14	70.0	288	9	BB177553	BB177553 BB177553
17	14	70.0	336	12	AQ660540	AQ660540 Sheared D
c 18	14	70.0	390	9	AV644609	AV644609 AV644609
19	14	70.0	416	9	AJ284239	AJ284239 4A3B-AAU-
20	14	70.0	421	12	AZ813806	AZ813806 2M0081E16
21	14	70.0	428	10	BM252718	BM252718 SnEST4a42
22	14	70.0	431	9	AW280184	AW280184 fj52a10.x
23	14	70.0	466	9	AF051116	AF051116 AF051116
c 24	14	70.0	472	10	BE449520	BE449520 EST356279
c 25	14	70.0	474	9	AV396989	AV396989 AV396989
c 26	14	70.0	476	9	AI483656	AI483656 EST249527
c 27	14	70.0	477	9	AI488127	AI488127 EST246449
28	14	70.0	489	9	AW618736	AW618736 EST320722
c 29	14	70.0	497	9	AV643117	AV643117 AV643117
c 30	14	70.0	508	9	AV642711	AV642711 AV642711
c 31	14	70.0	518	9	AV642141	AV642141 AV642141
c 32	14	70.0	525	9	AW650840	AW650840 EST329294
c 33	14	70.0	531	9	AV642766	AV642766 AV642766
34	14	70.0	544	12	AQ843909	AQ843909 LMAJFV1_1
c 35	14	70.0	556	9	AW155814	AW155814 614097B10
c 36	14	70.0	562	12	BH487728	BH487728 BOGQP76TR
c 37	14	70.0	566	9	AV631818	AV631818 AV631818
c 38	14	70.0	582	12	CNS01K68	AL147937 Anopheles
39	14	70.0	626	9	AW442770	AW442770 EST307700
c 40	14	70.0	626	9	BB640393	BB640393 BB640393
41	14	70.0	628	10	BF270176	BF270176 GA__Eb000
42	14	70.0	664	10	BG102752	BG102752 RHI22_36_
43	14	70.0	670	12	AQ943645	AQ943645 Sheared D
c 44	14	70.0	672	12	AQ943372	AQ943372 Sheared D
c 45	14	70.0	676	9	AI491107	AI491107 EST241816

ALIGNMENTS

RESULT 1
W06754/c
LOCUS W06754 234 bp mRNA linear EST 01-JUL-1996
DEFINITION SMEST0390 Schistosoma mansoni, adult worm, Gloria Franco
Schistosoma mansoni cDNA clone SMPBE73 3' end, mRNA sequence.
ACCESSION W06754
VERSION W06754.1 GI:1444974
KEYWORDS EST.
SOURCE Schistosoma mansoni.
ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE 1 (bases 1 to 234)
AUTHORS Franco,G.R. and Pena,S.D.J.
TITLE Franco,G.R. and Pena,S.D.J., Unpublished
JOURNAL Unpublished (1996)
COMMENT Contact: Franco G.R. and Pena S.D.J.
Laboratorio de Genetica-Bioquimica, Departamento de Bioquimicae Imunologia
Instituto de Ciencias Biologicas, Universidade Federal de Minas Gerais
Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
Tel: (5531)4415611
Fax: (5531)4415409
Email: gfranco@mono.icb.ufmg.br
Seq primer: M13 Forward.
FEATURES Location/Qualifiers
source 1. .234
/organism="Schistosoma mansoni"
/strain="NMRI"
/db_xref="taxon:6183"
/clone="SMPBE73"
/clone_lib="Schistosoma mansoni, adult worm, Gloria Franco"
/lab_host="DH10B, JM109"
/note="Vector: BA vector; Site_1: NotI; Site_2: HindIII; Total cellular RNA from male and female adult worms was extracted according to a modification (Puissant, C. and Houdebine, L. M. BioFeedback 8, 148-149, 1990) of the Guanidine Thiocyanate procedure (Chomczynski, P. and

Sacchi, N. Anal. Biochem. 162, 156- 159, 1987). Poly (A)+ RNA was purified by oligo dT column and cDNA was synthesized as described previously (Adams, M. D. et al. Nature Genet. 4, 373-389, 1993). cDNA was ligated to a two fold molar excess of a NotI/HindIII digested plasmid DNA (lafmid BA vector, a phagemid derived from pEMBL, Adams, M. D. et al. Nature Genet. 4, 373-389, 1993)) and electroporated into E. coli strain DH10B (BRL). The library was amplified and further selected for clones containing long inserts (>500 bp) by purification of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel, containing the smear of the library and electroporation into DH10B cells. "

BASE COUNT 49 a 84 c 66 g 33 t 2 others
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 234;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaa 17
||||||||||||||||||
Db 64 TACGGCGTTTCGATGAA 48

RESULT 2
T24127/c
LOCUS T24127 579 bp mRNA linear EST 27-FEB-1995
DEFINITION SMEST0325 Schistosoma mansoni, adult worm, Gloria Franco Schistosoma mansoni cDNA clone SMPBC65 3', mRNA sequence.
ACCESSION T24127
VERSION T24127.1 GI:529730
KEYWORDS EST.
SOURCE Schistosoma mansoni.
ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE 1 (bases 1 to 579)
AUTHORS Franco,G.R., Adams,M.D., Soares,M.B., Simpson,A.J.G., Venter,J.C. and Pena,S.D.J.
TITLE Identification of new Schistosoma mansoni genes by the EST strategy using a directional cDNA library
JOURNAL Gene 152, 141-147 (1995)
MEDLINE 95137379
COMMENT Contact: Franco G.R. and Pena S.D.J.
Laboratorio de Genetica-Bioquimica, Departamento de Bioquimicae Imunologia
Instituto de Ciencias Biologicas, Universidade Federal de Minas Gerais
Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
Tel: (5531)4415611
Fax: (5531)4415409
Email: gfranco@mono.icb.ufmg.br
Seq primer: M13 Forward.
FEATURES Location/Qualifiers
source 1. .579
/organism="Schistosoma mansoni"
/strain="NMRI"
/db_xref="taxon:6183"
/clone="SMPBC65"
/clone_lib="Schistosoma mansoni, adult worm, Gloria Franco"
/lab_host="DH10B, JM109"
/note="Vector: BA vector; Site_1: NotI; Site_2: HindIII; Total cellular RNA from male and female adult worms was extracted according to a modification (Puissant, C. and Houdebine, L. M. BioFeedback 8, 148-149, 1990) of the Guanidine Thiocyanate procedure (Chomczynski, P. and Sacchi, N. Anal. Biochem. 162, 156- 159, 1987). Poly (A)+ RNA was purified by oligo dT column and cDNA was synthesized as described previously (Adams, M. D. et al. Nature Genet. 4, 373-389, 1993). cDNA was ligated to a two fold molar excess of a NotI/HindIII digested plasmid DNA (lafmid BA vector, a phagemid derived from pEMBL, Adams, M. D. et al. Nature Genet. 4, 373-389, 1993)) and electroporated into E. coli strain DH10B (BRL). The library was amplified and further selected for clones containing long inserts (>500 bp) by purification of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel, containing the smear of the library and electroporation into DH10B cells. "

BASE COUNT 102 a 206 c 179 g 88 t 4 others
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaa 17
||||||||||||||||||
Db 75 TACGGCGTTTCGATGAA 59

RESULT 3
BE896357
LOCUS BE896357 624 bp mRNA linear EST 20-OCT-2000
DEFINITION 601439015F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924266 5', mRNA sequence.
ACCESSION BE896357
VERSION BE896357.1 GI:10360678
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 624)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9761 row: m column: 03
High quality sequence start: 2
High quality sequence stop: 403.
FEATURES Location/Qualifiers
source 1. .624
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3924266"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."
BASE COUNT 155 a 209 c 150 g 110 t
ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 624;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 gcgtttcgatgaaccc 20
||||||||||||||||
Db 582 GCGTTTCGATGAACCC 597

```
RESULT   4
BM077908
LOCUS       BM077908                384 bp    mRNA    linear   EST 14-NOV-2001
DEFINITION  pb21g06.y1 Ancylostoma caninum L3 SS SL1 TOPO v1 Murphy Chiapelli
            McCarter Ancylostoma caninum cDNA 5', mRNA sequence.
ACCESSION   BM077908
VERSION     BM077908.1  GI:16924944
KEYWORDS    EST.
SOURCE      dog hookworm.
  ORGANISM  Ancylostoma caninum
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
            Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
REFERENCE   1  (bases 1 to 384)
  AUTHORS   McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.
            , Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.
            , Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R.
            , Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
            ,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.
            , Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
            Wilson,R.
  TITLE     The Washington Univ. Nematode EST Project, 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: McCarter JP
            The Washington Univ. Nematode EST Project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            The library was constructed by Claire Murphy, Brandi Chiapelli, and
            Dr. James McCarter at Washington University, St. Louis. DNA
            Sequencing by: Washington University Genome Sequencing Center.
FEATURES             Location/Qualifiers
     source          1. .384
                     /organism="Ancylostoma caninum"
                     /db_xref="taxon:29170"
                     /clone_lib="Ancylostoma caninum L3 SS SL1 TOPO v1 Murphy
                     Chiapelli McCarter"
                     /dev_stage="Serum stimulated L3"
                     /lab_host="DH10B"
                     /note="Vector: pCRII-TOPO (Invitrogen); Site_1: EcoRI;
                     Site_2: EcoRI; The library was constructed by Claire
                     Murphy, Brandi Chiapelli,  and Dr. James McCarter at
                     Washington University, St. Louis. Oligo(dT)-SL1  PCR based
                     library. Ancylostoma caninum SS/L3 cDNA PCR products of
                     size  >400 nucleotides containing SL1 on the 5' end and
                     oligo(dT) on the 3' end  were non-directionally cloned
                     into pCRII-TOPO(Invitrogen) following the  Topo TA cloning
                     protocol. Nematodes were provided by Dr. Prema Arasu
                     (Prema_Arasu@ncsu.edu) of North Carolina State University
                     in Raleigh, NC."
BASE COUNT      116 a     71 c     85 g    112 t
ORIGIN


  Query Match           75.0%;  Score 15;  DB 10;  Length 384;
  Best Local Similarity  100.0%;  Pred. No. 39;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 ggcgtttcgatgaac 18
           ||||||||||||||||
Db     324 GGCGTTTCGATGAAC 338


RESULT   5
AW694629/c
LOCUS       AW694629                452 bp    mRNA    linear   EST 21-DEC-2000
DEFINITION  NF078E03ST1F1021 Developing stem Medicago truncatula cDNA clone
            NF078E03ST 5', mRNA sequence.
ACCESSION   AW694629
VERSION     AW694629.2  GI:11957636
KEYWORDS    EST.
SOURCE      barrel medic.
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 452)
  AUTHORS   He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
            ,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
            ,R.A.
  TITLE     Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula stem library
  JOURNAL   Unpublished (2000)
COMMENT     On Apr 14, 2000 this sequence version replaced gi:7569391.
            Contact: Dixon RA
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7302
            Fax: 580 221 7380
            Email: radixon@noble.org
            Insert Length: 736   Std Error: 0.00
            Plate: 078  row: E  column: 03
            Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
     source          1. .452
                     /organism="Medicago truncatula"
                     /db_xref="taxon:3880"
                     /clone="NF078E03ST"
                     /clone_lib="Developing stem"
                     /tissue_type="stem"
                     /dev_stage="Pooled developmental"
                     /note="Vector: Lambda Zap; Contains a mixture of
                     internodal stem segments"
BASE COUNT      152 a     94 c     91 g    115 t
ORIGIN


  Query Match           75.0%;  Score 15;  DB 9;  Length 452;
  Best Local Similarity  100.0%;  Pred. No. 40;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 cgtttcgatgaaccc 20
           |||||||||||||||
Db     338 CGTTTCGATGAACCC 324


RESULT   6
TA247H04P
LOCUS       TA247H04P               517 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 247h04, forward sequence,
            genomic survey sequence.
ACCESSION   AL483262
VERSION     AL483262.1  GI:11848938
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei.
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 517)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
```

4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES Location/Qualifiers
source 1. .517
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="247h04"
BASE COUNT 116 a 116 c 135 g 150 t
ORIGIN

Query Match 75.0%; Score 15; DB 12; Length 517;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ggcgtttcgatgaac 18
||||||||||||||||
Db 293 GGCGTTTCGATGAAC 307

RESULT 7
AQ783856
LOCUS AQ783856 536 bp DNA linear GSS 03-AUG-1999
DEFINITION HS_2001_A2_F09_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=18 Row=K, DNA sequence.
ACCESSION AQ783856
VERSION AQ783856.1 GI:5691480
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 536)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2001 row: K column: 18
Seq primer: T7
Class: BAC ends
High quality sequence stop: 536.
FEATURES Location/Qualifiers
source 1. .536
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=2001 Col=18 Row=K"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
BASE COUNT 160 a 124 c 92 g 156 t 4 others
ORIGIN

Query Match 75.0%; Score 15; DB 12; Length 536;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 cgtttcgatgaaccc 20
|||||||||||||||
Db 506 CGTTTCGATGAACCC 520

RESULT 8
TA140G03P
LOCUS TA140G03P 537 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 140g03, forward sequence, genomic survey sequence.
ACCESSION AL466454
VERSION AL466454.1 GI:11835809
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 537)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES Location/Qualifiers
source 1. .537
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="140g03"
BASE COUNT 108 a 120 c 110 g 199 t
ORIGIN

Query Match 75.0%; Score 15; DB 12; Length 537;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ggcgtttcgatgaac 18
||||||||||||||||
Db 85 GGCGTTTCGATGAAC 99

RESULT 9
TA190A10P/c
LOCUS TA190A10P 540 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 190a10, forward sequence, genomic survey sequence.
ACCESSION AL477985
VERSION AL477985.1 GI:11841795
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

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REFERENCE   1  (bases 1 to 540)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nhl@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .540
                     /organism="Trypanosoma brucei"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="190a10"
BASE COUNT      177 a    118 c    126 g    119 t
ORIGIN


  Query Match             75.0%;  Score 15;  DB 12;  Length 540;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggcgtttcgatgaac 18
          ||||||||||||||||
Db    325 GGCGTTTCGATGAAC 311


RESULT  10
BH615799
LOCUS       BH615799                631 bp    DNA     linear   GSS 28-JAN-2002
DEFINITION  BMBAC304F01SP6_PSU Brugia malayi Genomic Bac Library 3 Brugia
            malayi genomic, DNA sequence.
ACCESSION   BH615799
VERSION     BH615799.1  GI:18380487
KEYWORDS    GSS.
SOURCE      Brugia malayi.
  ORGANISM  Brugia malayi
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Brugia.
REFERENCE   1  (bases 1 to 631)
  AUTHORS   Whitton,C., Daub,J., Ware,J., Quail,M., Hall,N., Barrell,B., Foster
            ,J., Guiliano,D., Slatko,B. and Blaxter,M.
  TITLE     Genome survey sequences from the human parasitic nematode Brugia
            malayi
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Blaxter ML
            Institute of Cell, Animal and Population Biology
            University of Edinburgh
            Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
            3JT, UK
            Tel: +44 131 650 6760
            Fax: +44 131 670 5450
            Email: mark.blaxter@ed.ac.uk
            Sequenced from the Brugia malayi BAC library constructed by Claire
            Whitton and Dr Mike Quail. The sequence was generated by The
            Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in
            collaboration with Mark Blaxter, ICAPB, University of Edinburgh,
            Edinburgh, UK.
            Seq primer: SP6 (ATTTAGGTGACACTATAG)
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .631
                     /organism="Brugia malayi"
                     /strain="TRS"
                     /db_xref="taxon:6279"
                     /clone_lib="Brugia malayi Genomic Bac Library 3"
                     /sex="Mixed (male and female)"
                     /tissue_type="whole parasite"
                     /dev_stage="microfilaria (L1)"
                     /note="Vector: pBACe3.6; Site_1: BamH I; Brugia malayi
                     genomic DNA was partially cleaved with Sau3A I and size
                     fractionated. 7,392 clones were generated with mean insert
                     size ~48 kbp. The library was constructed by Claire
                     Whitton, Blaxter Nematode Genetics Lab, University of
                     Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing
                     Unit, The Sanger Centre, Cambridge, UK."
BASE COUNT      196 a     94 c    142 g    199 t
ORIGIN


  Query Match             75.0%;  Score 15;  DB 12;  Length 631;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 acggcgtttcgatga 16
          ||||||||||||||||
Db    606 ACGGCGTTTCGATGA 620


RESULT  11
BE053145
LOCUS       BE053145                690 bp    mRNA    linear   EST 07-MAR-2001
DEFINITION  GA__Ea0002K16f Gossypium arboreum 7-10 dpa fiber library Gossypium
            arboreum cDNA clone GA__Ea0002K16f, mRNA sequence.
ACCESSION   BE053145
VERSION     BE053145.2  GI:13244065
KEYWORDS    EST.
SOURCE      Gossypium arboreum.
  ORGANISM  Gossypium arboreum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
REFERENCE   1  (bases 1 to 690)
  AUTHORS   Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
            ,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
  TITLE     An integrated analysis of the genetics, development, and evolution
            of the cotton fiber
  JOURNAL   Unpublished (2000)
COMMENT     On Jun 8, 2000 this sequence version replaced gi:8380201.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Seq primer: TAATACGACTCACTATAGGG
            High quality sequence stop: 550.
FEATURES             Location/Qualifiers
     source          1. .690
                     /organism="Gossypium arboreum"
                     /strain="AKA"
                     /cultivar="8400"
                     /db_xref="taxon:29729"
                     /clone="GA__Ea0002K16f"
                     /clone_lib="Gossypium arboreum 7-10 dpa fiber library"
                     /tissue_type="Fibers isolated from bolls harvested 7-10
                     dpa"
                     /lab_host="E. coli"
                     /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT      169 a    132 c    151 g    236 t      2 others
ORIGIN
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  Query Match             75.0%;  Score 15;  DB 9;  Length 690;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggcgtttcgatgaac 18
          ||||||||||||||||
Db    567 GGCGTTTCGATGAAC 581


RESULT 12
CNS040YP/c
LOCUS       CNS040YP                1033 bp    DNA     linear   GSS 18-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            073004 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL269530
VERSION     AL269530.1  GI:7991421
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 1033)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1033)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1033)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .1033
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="073004"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0BG073BH02LP1~end : T7"
BASE COUNT      270 a    222 c    276 g    261 t      4 others
ORIGIN


  Query Match             75.0%;  Score 15;  DB 12;  Length 1033;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 cggcgtttcgatgaa 17
          |||||||||||||||
Db    460 CGGCGTTTCGATGAA 446


RESULT 13
BM007170
LOCUS       BM007170                1218 bp    mRNA    linear   EST 30-OCT-2001
DEFINITION  603614933T1 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:5420816 3',
            mRNA sequence.
ACCESSION   BM007170
VERSION     BM007170.1  GI:16521524
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1218)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1876  row: a  column: 09
            High quality sequence start: 25
            High quality sequence stop: 313.
FEATURES             Location/Qualifiers
     source          1. .1218
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5420816"
                     /clone_lib="NIH_MGC_110"
                     /tissue_type="ductal carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      370 a    446 c    244 g    154 t      4 others
ORIGIN


  Query Match             75.0%;  Score 15;  DB 10;  Length 1218;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 cgtttcgatgaaccc 20
          |||||||||||||||
Db    364 CGTTTCGATGAACCC 378


RESULT 14
AV640031/c
LOCUS       AV640031                 247 bp    mRNA    linear   EST 15-DEC-2000
DEFINITION  AV640031 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii
            cDNA clone HCL009b04_r 5', mRNA sequence.
ACCESSION   AV640031
VERSION     AV640031.1  GI:10783359
KEYWORDS    EST.
SOURCE      Chlamydomonas reinhardtii.
  ORGANISM  Chlamydomonas reinhardtii
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
            Chlamydomonadaceae; Chlamydomonas.
REFERENCE   1  (bases 1 to 247)
  AUTHORS   Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
            Nakamura,Y. and Tabata,S.
  TITLE     Generation of expressed sequence tags from low-CO2 and high-CO2
            adapted cells of Chlamydomonas reinhardtii
  JOURNAL   DNA Res. 7 (5), 305-307 (2000)
  MEDLINE   20539644
COMMENT     Contact: Erika Asamizu
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
```

```
           Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
           Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES             Location/Qualifiers
     source          1. .247
                     /organism="Chlamydomonas reinhardtii"
                     /strain="C9"
                     /db_xref="taxon:3055"
                     /clone="HCL009b04_r"
                     /clone_lib="Chlamydomonas reinhardtii 5% CO2"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI; The cDNA library was constructed from cells cultured
                     in a medium with bubbling air containing 5% carbon
                     dioxide"
BASE COUNT       61 a     79 c     54 g     53 t
ORIGIN


  Query Match             70.0%;  Score 14;  DB 9;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggcgtttcgatgaa 17
          ||||||||||||||
Db    245 GGCGTTTCGATGAA 232


RESULT 15
AV640876/c
LOCUS       AV640876                 269 bp    mRNA    linear   EST 15-DEC-2000
DEFINITION  AV640876 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii
            cDNA clone HCL024a01_r 5', mRNA sequence.
ACCESSION   AV640876
VERSION     AV640876.1  GI:10784204
KEYWORDS    EST.
SOURCE      Chlamydomonas reinhardtii.
  ORGANISM  Chlamydomonas reinhardtii
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
            Chlamydomonadaceae; Chlamydomonas.
REFERENCE   1  (bases 1 to 269)
  AUTHORS   Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
            Nakamura,Y. and Tabata,S.
  TITLE     Generation of expressed sequence tags from low-CO2 and high-CO2
            adapted cells of Chlamydomonas reinhardtii
  JOURNAL   DNA Res. 7 (5), 305-307 (2000)
  MEDLINE   20539644
COMMENT     Contact: Erika Asamizu
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES             Location/Qualifiers
     source          1. .269
                     /organism="Chlamydomonas reinhardtii"
                     /strain="C9"
                     /db_xref="taxon:3055"
                     /clone="HCL024a01_r"
                     /clone_lib="Chlamydomonas reinhardtii 5% CO2"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI; The cDNA library was constructed from cells cultured
                     in a medium with bubbling air containing 5% carbon
                     dioxide"
BASE COUNT       65 a     85 c     60 g     59 t
ORIGIN


  Query Match             70.0%;  Score 14;  DB 9;  Length 269;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggcgtttcgatgaa 17
          ||||||||||||||
Db    254 GGCGTTTCGATGAA 241


Search completed: August  7, 2002, 23:12:33
Job time: 11072 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:54:21 ; Search time 146.61 Seconds
(without alignments)
33.508 Million cell updates/sec

Title: US-09-786-105-4
Perfect score: 20
Sequence: 1 tacggcgtttcgatgaaccc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	20	100.0	432	2	US-08-313-185-59	Sequence 59, Appl
c	2	20	100.0	432	3	US-09-082-614A-59	Sequence 59, Appl
c	3	20	100.0	620	2	US-08-757-653-135	Sequence 135, App
c	4	20	100.0	620	2	US-08-757-653-136	Sequence 136, App
c	5	20	100.0	620	2	US-08-757-653-137	Sequence 137, App
	6	20	100.0	620	2	US-08-757-653-138	Sequence 138, App
	7	20	100.0	620	2	US-08-757-653-139	Sequence 139, App
	8	20	100.0	620	2	US-08-757-653-140	Sequence 140, App
c	9	20	100.0	706	4	US-08-797-812-24	Sequence 24, Appl
c	10	20	100.0	970	1	US-08-250-030-1	Sequence 1, Appli
c	11	20	100.0	970	5	PCT-US95-06790-1	Sequence 1, Appli
	12	19	95.0	19	4	US-08-750-088A-71	Sequence 71, Appl
c	13	18.4	92.0	3447	2	US-08-313-185-57	Sequence 57, Appl
c	14	18.4	92.0	3447	3	US-09-082-614A-57	Sequence 57, Appl
c	15	15.8	79.0	1472	1	US-08-622-354-2	Sequence 2, Appli
c	16	15.8	79.0	2310	1	US-08-622-354-1	Sequence 1, Appli
	17	15.2	76.0	4403765	4	US-09-103-840A-2	Sequence 2, Appli
	18	15	75.0	27	1	US-08-250-030-9	Sequence 9, Appli
	19	15	75.0	27	5	PCT-US95-06790-9	Sequence 9, Appli
	20	14.2	71.0	1081	4	US-09-372-422A-33	Sequence 33, Appl
	21	14.2	71.0	1153	4	US-09-372-448A-5	Sequence 5, Appli
	22	14.2	71.0	2262	2	US-08-674-887A-5	Sequence 5, Appli
	23	14.2	71.0	2262	3	US-08-951-844-5	Sequence 5, Appli
c	24	13.8	69.0	117	1	US-08-299-498A-59	Sequence 59, Appl
c	25	13.8	69.0	117	5	PCT-US95-10813-59	Sequence 59, Appl
	26	13.8	69.0	776	4	US-09-372-422A-43	Sequence 43, Appl
	27	13.8	69.0	1100	4	US-09-372-422A-47	Sequence 47, Appl
c	28	13.8	69.0	1176	3	US-08-911-853-34	Sequence 34, Appl
c	29	13.8	69.0	1176	4	US-09-479-409-34	Sequence 34, Appl
c	30	13.8	69.0	1176	4	US-09-479-453-34	Sequence 34, Appl
	31	13.8	69.0	1375	4	US-09-372-422A-37	Sequence 37, Appl
	32	13.8	69.0	1485	4	US-09-372-422A-39	Sequence 39, Appl
	33	13.8	69.0	2394	3	US-09-027-064-1	Sequence 1, Appli
	34	13.8	69.0	2394	4	US-09-271-815-1	Sequence 1, Appli
c	35	13.8	69.0	17612	3	US-08-911-853-29	Sequence 29, Appl
c	36	13.8	69.0	17612	4	US-09-479-409-29	Sequence 29, Appl
c	37	13.8	69.0	17612	4	US-09-479-453-29	Sequence 29, Appl
c	38	13.8	69.0	4403765	4	US-09-103-840A-2	Sequence 2, Appli
	39	13.6	68.0	585	4	US-09-404-671-3	Sequence 3, Appli
	40	13.6	68.0	686	4	US-09-372-422A-45	Sequence 45, Appl
c	41	13.6	68.0	699	4	US-08-998-416-705	Sequence 705, App
c	42	13.6	68.0	999	4	US-09-177-234-7	Sequence 7, Appli
	43	13.6	68.0	1087	4	US-09-372-422A-29	Sequence 29, Appl
	44	13.6	68.0	1209	1	US-08-314-309A-5	Sequence 5, Appli
	45	13.6	68.0	1513	1	US-08-314-309A-2	Sequence 2, Appli

ALIGNMENTS

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RESULT   1
US-08-313-185-59/c
; Sequence 59, Application US/08313185
; Patent No. 5851763
;  GENERAL INFORMATION:
;    APPLICANT:  Heym, Beate
;    APPLICANT:  Cole, Stewart
;    APPLICANT:  Young, Douglas
;    APPLICANT:  Zhang, Ying
;    APPLICANT:  Honore, Nadine
;    APPLICANT:  Telenti, Amalio
;    APPLICANT:  Bodmer, Thomas
;    TITLE OF INVENTION:  Rapid Detection of Antibiotic Resistance
;    TITLE OF INVENTION:  in Mycobacterium Tuberculosis
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/313,185
;      FILING DATE:  12-OCT-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  02356.0068-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-313-185-59


  Query Match             100.0%;  Score 20;  DB 2;  Length 432;
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  Best Local Similarity   100.0%;  Pred. No. 0.033;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
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Db     428 TACGGCGTTTCGATGAACCC 409


RESULT   2
US-09-082-614A-59/c
; Sequence 59, Application US/09082614A
; Patent No. 6124098
;  GENERAL INFORMATION:
;    APPLICANT:  Heym, Beate
;    APPLICANT:  Cole, Stewart
;    APPLICANT:  Young, Douglas
;    APPLICANT:  Zhang, Ying
;    APPLICANT:  Honore, Nadine
;    APPLICANT:  Telenti, Amalio
;    APPLICANT:  Bodmer, Thomas
;    TITLE OF INVENTION:  Rapid Detection of Antibiotic Resistance
;    TITLE OF INVENTION:  in Mycobacterium Tuberculosis
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/082,614A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/313,185
;      FILING DATE:  12-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  02356.0068-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-082-614A-59


  Query Match             100.0%;  Score 20;  DB 3;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 0.033;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
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Db     428 TACGGCGTTTCGATGAACCC 409


RESULT   3
US-08-757-653-135/c
; Sequence 135, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  135:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-135


  Query Match             100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity   100.0%;  Pred. No. 0.034;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
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Db     296 TACGGCGTTTCGATGAACCC 277


RESULT   4
US-08-757-653-136/c
; Sequence 136, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
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;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  136:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-136


  Query Match           100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity  100.0%;  Pred. No. 0.034;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    296 TACGGCGTTTCGATGAACCC 277


RESULT   5
US-08-757-653-137/c
; Sequence 137, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  137:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-137


  Query Match           100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity  100.0%;  Pred. No. 0.034;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    296 TACGGCGTTTCGATGAACCC 277


RESULT   6
US-08-757-653-138
; Sequence 138, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  138:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-138


  Query Match           100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity  100.0%;  Pred. No. 0.034;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    325 TACGGCGTTTCGATGAACCC 344


RESULT   7
US-08-757-653-139
; Sequence 139, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  139:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-139


  Query Match             100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity   100.0%;  Pred. No. 0.034;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
           ||||||||||||||||||||
Db     325 TACGGCGTTTCGATGAACCC 344


RESULT   8
US-08-757-653-140
; Sequence 140, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  140:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-140


  Query Match             100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity   100.0%;  Pred. No. 0.034;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
           ||||||||||||||||||||
Db     325 TACGGCGTTTCGATGAACCC 344


RESULT   9
US-08-797-812-24/c
; Sequence 24, Application US/08797812
; Patent No. 6228575
;  GENERAL INFORMATION:
;    APPLICANT:  Gingeras, Thomas A.
;    APPLICANT:  Mack, David
;    APPLICANT:  Chee, Mark S.
;    APPLICANT:  Berno, Anthony J.
;    APPLICANT:  Stryer, Lubert
;    APPLICANT:  Ghandour, Ghassan
;    APPLICANT:  Wang, Ching
;    TITLE OF INVENTION:  Chip-Based Species Identification and
;    TITLE OF INVENTION:  Phenotypic Characterization of Microorganisms
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/797,812
;      FILING DATE:  07-FEB-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/017,765
;      FILING DATE:  15-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/629,031
;      FILING DATE:  08-APR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/012,631
;      FILING DATE:  01-MAR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,339
;      FILING DATE:  08-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitts, Renee A.
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16528X-018550
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  24:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  706 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-797-812-24


  Query Match            100.0%;  Score 20;  DB 4;  Length 706;
  Best Local Similarity   100.0%;  Pred. No. 0.035;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    332 TACGGCGTTTCGATGAACCC 313


RESULT  10
US-08-250-030-1/c
; Sequence 1, Application US/08250030
; Patent No. 5643723
;  GENERAL INFORMATION:
;    APPLICANT:  Persing, David H.
;    TITLE OF INVENTION:  Detection of a Genetic Locus Encoding
;    TITLE OF INVENTION:  Resistance to Rifampin in Mycobacterial Cultures and in
;    TITLE OF INVENTION:  Clinical Specimens
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schwegman, Lundberg & Woessner
;      STREET:  3500 IDS Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/250,030
;      FILING DATE:  26-MAY-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueting, Ann M.
;      REGISTRATION NUMBER:  33,977
;      REFERENCE/DOCKET NUMBER:  150.105US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-339-0331
;      TELEFAX:  612-339-3061
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  970 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-250-030-1


  Query Match            100.0%;  Score 20;  DB 1;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 0.036;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    671 TACGGCGTTTCGATGAACCC 652


RESULT  11
PCT-US95-06790-1/c
; Sequence 1, Application PC/TUS9506790
;  GENERAL INFORMATION:
;    APPLICANT:  Mayo Foundation for Medical Education and Research
;    APPLICANT:  and Hoffmann-La Roche Inc.
;    TITLE OF INVENTION:  Detection of a Genetic Locus Encoding
;    TITLE OF INVENTION:  Resistance to Rifampin
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schwegman, Lundberg & Woessner
;      STREET:  3500 IDS Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/06790
;      FILING DATE:  26-MAY-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Raasch, Kevin W.
;      REGISTRATION NUMBER:  35,651
;      REFERENCE/DOCKET NUMBER:  150.105WO1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-339-0331
;      TELEFAX:  612-339-3061
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  970 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
PCT-US95-06790-1


  Query Match            100.0%;  Score 20;  DB 5;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 0.036;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    671 TACGGCGTTTCGATGAACCC 652


RESULT  12
US-08-750-088A-71
; Sequence 71, Application US/08750088A
; Patent No. 6329138
;  GENERAL INFORMATION:
;    APPLICANT:  DE BEENHOUWER, HANS
;    APPLICANT:  PORTAELS, FRAN OISE
;    APPLICANT:  MACHTELINCKX, LIEVE
;    APPLICANT:  JANNES, GEERT
;    APPLICANT:  ROSSAU, RUDI
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF THE ANTIBIOTIC
;    TITLE OF INVENTION:  RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  US
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/750,088A
;      FILING DATE:  21-FEB-1997
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GOLDSTEIN, JORGE A.
;      REGISTRATION NUMBER:  29,021
;      REFERENCE/DOCKET NUMBER:  1657.0010000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-750-088A-71


  Query Match            95.0%;  Score 19;  DB 4;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 0.08;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaacc 19
          |||||||||||||||||||
Db      1 TACGGCGTTTCGATGAACC 19


RESULT  13
US-08-313-185-57/c
; Sequence 57, Application US/08313185
; Patent No. 5851763
;  GENERAL INFORMATION:
;    APPLICANT:  Heym, Beate
;    APPLICANT:  Cole, Stewart
;    APPLICANT:  Young, Douglas
;    APPLICANT:  Zhang, Ying
;    APPLICANT:  Honore, Nadine
;    APPLICANT:  Telenti, Amalio
;    APPLICANT:  Bodmer, Thomas
;    TITLE OF INVENTION:  Rapid Detection of Antibiotic Resistance
;    TITLE OF INVENTION:  in Mycobacterium Tuberculosis
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/313,185
;      FILING DATE:  12-OCT-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  02356.0068-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3447 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-313-185-57


  Query Match            92.0%;  Score 18.4;  DB 2;  Length 3447;
  Best Local Similarity  95.0%;  Pred. No. 0.32;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||| ||||||||||||||
Db   1454 TACGGTGTTTCGATGAACCC 1435


RESULT  14
US-09-082-614A-57/c
; Sequence 57, Application US/09082614A
; Patent No. 6124098
;  GENERAL INFORMATION:
;    APPLICANT:  Heym, Beate
;    APPLICANT:  Cole, Stewart
;    APPLICANT:  Young, Douglas
;    APPLICANT:  Zhang, Ying
;    APPLICANT:  Honore, Nadine
;    APPLICANT:  Telenti, Amalio
;    APPLICANT:  Bodmer, Thomas
;    TITLE OF INVENTION:  Rapid Detection of Antibiotic Resistance
;    TITLE OF INVENTION:  in Mycobacterium Tuberculosis
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/082,614A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/313,185
;      FILING DATE:  12-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  02356.0068-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3447 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-082-614A-57


  Query Match            92.0%;  Score 18.4;  DB 3;  Length 3447;
  Best Local Similarity  95.0%;  Pred. No. 0.32;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||| ||||||||||||||
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Db   1454 TACGGTGTTTCGATGAACCC 1435


RESULT 15
US-08-622-354-2/c
; Sequence 2, Application US/08622354
; Patent No. 5827518
;  GENERAL INFORMATION:
;    APPLICANT:  WEBB, Bruce A.
;    APPLICANT:  CUI, Liwang
;    TITLE OF INVENTION:  VIRAL AND INSECT GENES THAT INHIBIT THE
;    TITLE OF INVENTION:  IMMUNE SYSTEM AND METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LOWE, PRICE, LEBLANC & BECKER
;      STREET:  99 Canal Center Plaza, Suite 300
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/622,354
;      FILING DATE:  27-MAR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Price, Robert L.
;      REGISTRATION NUMBER:  22,685
;      REFERENCE/DOCKET NUMBER:  434-061
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 684-1111
;      TELEFAX:  (703) 684-1124
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1472 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  190..1155
US-08-622-354-2


  Query Match           79.0%;  Score 15.8;  DB 1;  Length 1472;
  Best Local Similarity  89.5%;  Pred. No. 8;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaacc 19
           ||||| |||| ||||||||
Db    1105 TACGGGGTTTAGATGAACC 1087


Search completed: August  7, 2002, 21:54:25
Job time: 24020 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:15:21 ; Search time 4103.44 Seconds
(without alignments)
65.784 Million cell updates/sec

Title: US-09-786-105-4
Perfect score: 20
Sequence: 1 tacggcgtttcgatgaaccc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		17.4	87.0	396	10	BF220419	BF220419 NXCI_146_
2		17.4	87.0	399	10	BF169611	BF169611 NXCI_125_
3		17.4	87.0	452	10	BG040291	BG040291 NXSI_110_
4		17.4	87.0	539	9	AA556698	AA556698 553 Loblo
5		17.4	87.0	545	10	BF777209	BF777209 NXSI_066_
6	c	17	85.0	234	10	W06754	W06754 SMEST0390 S
7	c	17	85.0	579	10	T24127	T24127 SMEST0325 S
8		16.8	84.0	277	9	AA734164	AA734164 vs19g12.r
9	c	16.4	82.0	576	10	BF252921	BF252921 EST420184
10		16.4	82.0	624	10	BE896357	BE896357 601439015
11		16.4	82.0	631	12	BH615799	BH615799 BMBAC304F
12	c	16.4	82.0	961	12	AG141490	AG141490 Pan trogl
13	c	15.8	79.0	213	9	AW064407	AW064407 SP0996 KR
14		15.8	79.0	436	9	AI496312	AI496312 sb05b08.y
15	c	15.8	79.0	582	12	CNS01K68	AL147937 Anopheles
16		15.8	79.0	637	10	BG908684	BG908684 TaLr1170D
17		15.8	79.0	650	10	BG908616	BG908616 TaLr1169H
18	c	15.8	79.0	752	12	CNS03678	AL229661 Tetraodon
19	c	15.8	79.0	775	12	AZ125549	AZ125549 OSJNBb009
20	c	15.8	79.0	885	12	CNS02B0Q	AL189251 Tetraodon
21	c	15.8	79.0	913	10	BF204833	BF204833 601867133
22	c	15.8	79.0	1029	12	CNS0549K	AL320465 Tetraodon
23	c	15.8	79.0	1411	10	BI663170	BI663170 603286791
24	c	15.6	78.0	885	12	CNS01K02	AL147715 Anopheles
25		15.4	77.0	248	10	BG140300	BG140300 EST480742
26	c	15.4	77.0	269	9	AV640876	AV640876 AV640876
27		15.4	77.0	384	10	BM077908	BM077908 pb21g06.y
28	c	15.4	77.0	390	9	AV644609	AV644609 AV644609
29		15.4	77.0	467	12	CNS03FUV	AL242176 Tetraodon
30	c	15.4	77.0	474	9	AV396989	AV396989 AV396989
31		15.4	77.0	489	9	AW618736	AW618736 EST320722
32	c	15.4	77.0	497	9	AV643117	AV643117 AV643117
33	c	15.4	77.0	508	9	AV642711	AV642711 AV642711
34	c	15.4	77.0	518	9	AV642141	AV642141 AV642141
35	c	15.4	77.0	531	9	AV642766	AV642766 AV642766
36		15.4	77.0	532	10	BI506216	BI506216 BB170018A
37		15.4	77.0	536	12	AQ783856	AQ783856 HS_2001_A
38		15.4	77.0	548	12	AQ497017	AQ497017 HS_5197_B
39	c	15.4	77.0	566	9	AV631818	AV631818 AV631818
40		15.4	77.0	788	10	BE566696	BE566696 601339653
41		15.2	76.0	146	10	BM096759	BM096759 EBma07_SQ
42		15.2	76.0	200	10	BM098906	BM098906 EBpi05_SQ
43		15.2	76.0	205	12	AZ577000	AZ577000 06d05 Sho
44		15.2	76.0	269	10	BF953380	BF953380 RC3-NN019
45		15.2	76.0	317	9	BB501888	BB501888 BB501888

ALIGNMENTS

RESULT 1
BF220419
LOCUS BF220419 396 bp mRNA linear EST 08-NOV-2000
DEFINITION NXCI_146_A06_F NXCI (Nsf Xylem Compression wood Inclined) Pinus taeda cDNA clone NXCI_146_A06 5', mRNA sequence.
ACCESSION BF220419
VERSION BF220419.1 GI:11126551
KEYWORDS EST.
SOURCE loblolly pine.
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 396)
AUTHORS Sederoff,R.
TITLE Molecular Basis of Wood Formation in the Pine Megagenome
JOURNAL Unpublished (2000)
COMMENT Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .396
/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NXCI_146_A06"
/clone_lib="NXCI (Nsf Xylem Compression wood Inclined)"
/tissue_type="Xylem"
/cell_type="Compression"
/dev_stage="Juvenile"
/lab_host="XL1-Blue"
/note="Vector: BlueScript SK; Site_1: Eco RI; Site_2: XhoI ; The library is from early (spring) wood, taken from three six-year old trees (three different genotypes), in the juvenile phase. These trees were induced to form compression wood by bending to a 45 degree angle and tying them to the ground. Differentiating xylem was harvested from the bottoms of the inclined stems, and a mixture of

all three genotypes was used for the library. oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI BlueScript SK vector arms. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGCACGAG'."
BASE COUNT 71 a 84 c 122 g 110 t 9 others
ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 396;
Best Local Similarity 94.7%; Pred. No. 71;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 acggcgtttcgatgaaccc 20
|||||| ||||||||||||
Db 15 ACGGCGCTTCGATGAACCC 33

RESULT 2
BF169611
LOCUS BF169611 399 bp mRNA linear EST 30-OCT-2000
DEFINITION NXCI_125_C05_F NXCI (Nsf Xylem Compression wood Inclined) Pinus taeda cDNA clone NXCI_125_C05 5', mRNA sequence.
ACCESSION BF169611
VERSION BF169611.1 GI:11054228
KEYWORDS EST.
SOURCE loblolly pine.
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 399)
AUTHORS Sederoff,R.
TITLE Molecular Basis of Wood Formation in the Pine Megagenome
JOURNAL Unpublished (2000)
COMMENT Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .399
/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NXCI_125_C05"
/clone_lib="NXCI (Nsf Xylem Compression wood Inclined)"
/tissue_type="Xylem"
/cell_type="Compression"
/dev_stage="Juvenile"
/lab_host="XL1-Blue"
/note="Vector: BlueScript SK; Site_1: Eco RI; Site_2: XhoI ; The library is from early (spring) wood, taken from three six-year old trees (three different genotypes), in the juvenile phase. These trees were induced to form compression wood by bending to a 45 degree angle and tying them to the ground. Differentiating xylem was harvested from the bottoms of the inclined stems, and a mixture of all three genotypes was used for the library. oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI BlueScript SK vector arms. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGCACGAG'."
BASE COUNT 71 a 84 c 121 g 121 t 2 others
ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 399;
Best Local Similarity 94.7%; Pred. No. 72;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 acggcgtttcgatgaaccc 20
|||||| ||||||||||||
Db 15 ACGGCGCTTCGATGAACCC 33

RESULT 3
BG040291
LOCUS BG040291 452 bp mRNA linear EST 24-JAN-2001
DEFINITION NXSI_110_F06_F NXSI (Nsf Xylem Side wood Inclined) Pinus taeda cDNA clone NXSI_110_F06 5', mRNA sequence.
ACCESSION BG040291
VERSION BG040291.1 GI:12482876
KEYWORDS EST.
SOURCE loblolly pine.
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 452)
AUTHORS Sederoff,R.
TITLE Molecular Basis of Wood Formation in the Pine Megagenome
JOURNAL Unpublished (2000)
COMMENT Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .452
/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NXSI_110_F06"
/clone_lib="NXSI (Nsf Xylem Side wood Inclined)"
/tissue_type="Xylem"
/cell_type="Side"
/dev_stage="Juvenile"
/lab_host="XL1-Blue"
/note="Vector: BlueScript SK; Site_1: Eco RI; Site_2: XhoI ; The library is from early (spring) wood, taken from three six-year old trees (three different genotypes), in the juvenile phase. These trees were induced to form side wood by bending to a 45 degree angle and tying them to the ground. Differentiating xylem was harvested from the sides of the inclined stems, and a mixture of all three genotypes was used for the library. oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI BlueScript SK vector arms. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGCACGAG'."
BASE COUNT 71 a 122 c 146 g 95 t 18 others
ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 452;
Best Local Similarity 94.7%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 acggcgtttcgatgaaccc 20
|||||| ||||||||||||
Db 329 ACGGCGCTTCGATGAACCC 347

RESULT 4
AA556698
LOCUS AA556698 539 bp mRNA linear EST 28-AUG-1998
DEFINITION 553 Loblolly pine CA Pinus taeda cDNA clone 1CAB4G, mRNA sequence.
ACCESSION AA556698
VERSION AA556698.1 GI:3365713
KEYWORDS EST.
SOURCE loblolly pine.
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 539)

```
  AUTHORS   Allona,I., Quinn,M., Shoop,E., Swope,K., St.Cyr,S., Carlis,J.,
            Riedl,J., Retzel,E, Campbell,M.M., Sederoff,R. and Whetten,R.W.
  TITLE     Analysis of xylem formation in pine by cDNA sequencing
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 95 (16), 9693-9698 (1998)
  MEDLINE   98356220
COMMENT     Contact: Ross Whetten
            Forest Biotechnology Group
            North Carolina State University
            Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
            ,NC, 27695-8008
            Tel: 919-515-7800
            Fax: 919-515-7801
            Email: rosswhet@unity.ncsu.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .539
                     /organism="Pinus taeda"
                     /strain="Coastal plain loblolly pine from North Carolina"
                     /db_xref="taxon:3352"
                     /clone="1CAB4G"
                     /clone_lib="Loblolly pine CA"
                     /tissue_type="Xylem"
                     /lab_host="SOLR"
                     /note="Vector: lambda-ZAP; Site_1: EcoRI; Site_2: XhoI;
                     The result of subtraction of C library with N library.
                     Immature xylem from the underside of inclined stems of
                     differentiating compression wood was subtracted with
                     immature xylem from the side of inclined stems of
                     differentiating wood. A mixture of four genotypes were
                     used. Oligo-dT primed cDNA was directionally cloned into
                     the EcoRI-XhoI lambda-ZAP vector arms"
BASE COUNT      102 a    120 c    156 g    150 t     11 others
ORIGIN


  Query Match             87.0%;  Score 17.4;  DB 9;  Length 539;
  Best Local Similarity   94.7%;  Pred. No. 78;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 acggcgtttcgatgaaccc 20
          |||||| ||||||||||||
Db    145 ACGGCGCTTCGATGAACCC 163


RESULT   5
BF777209
LOCUS       BF777209                 545 bp    mRNA    linear   EST 12-JAN-2001
DEFINITION  NXSI_066_E05_F NXSI (Nsf Xylem Side wood Inclined) Pinus taeda cDNA
            clone NXSI_066_E05 5', mRNA sequence.
ACCESSION   BF777209
VERSION     BF777209.1  GI:12125109
KEYWORDS    EST.
SOURCE      loblolly pine.
  ORGANISM  Pinus taeda
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE   1  (bases 1 to 545)
  AUTHORS   Sederoff,R.
  TITLE     Molecular Basis of Wood Formation in the Pine Megagenome
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Johnson, Arthur
            North Carolina State University
            Tel: 919 515 7800
            Fax: 919 515 7801
            Email: ajohnson@unity.ncsu.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .545
                     /organism="Pinus taeda"
                     /strain="Coastal plain loblolly pine from North Carolina"
                     /db_xref="taxon:3352"
                     /clone="NXSI_066_E05"
                     /clone_lib="NXSI (Nsf Xylem Side wood Inclined)"
                     /tissue_type="Xylem"
                     /cell_type="Side"
                     /dev_stage="Juvenile"
                     /lab_host="XL1-Blue"
                     /note="Vector: BlueScript SK; Site_1: Eco RI; Site_2: XhoI
                     ; The library is from early (spring) wood, taken from
                     three six-year old trees (three different genotypes), in
                     the juvenile phase. These trees were induced to form side
                     wood by bending to a 45 degree angle and tying them to the
                     ground. Differentiating xylem was harvested from the sides
                     of the inclined stems, and a mixture of all three
                     genotypes was used for the library. oligo-dT primed cDNA
                     was directionally cloned into the EcoRI-XhoI BlueScript SK
                     vector arms. NOTE: The sequences contain a 'cDNA adapter'
                     between the EcoRI site and the start of the EST. The
                     adapter sequence is 'AATTCGGCACGAG'."
BASE COUNT      92 a    142 c    167 g    132 t     12 others
ORIGIN


  Query Match             87.0%;  Score 17.4;  DB 10;  Length 545;
  Best Local Similarity   94.7%;  Pred. No. 78;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 acggcgtttcgatgaaccc 20
          |||||| ||||||||||||
Db    256 ACGGCGCTTCGATGAACCC 274


RESULT   6
W06754/c
LOCUS       W06754                   234 bp    mRNA    linear   EST 01-JUL-1996
DEFINITION  SMEST0390 Schistosoma mansoni, adult worm, Gloria Franco
            Schistosoma mansoni cDNA clone SMPBE73 3' end, mRNA sequence.
ACCESSION   W06754
VERSION     W06754.1  GI:1444974
KEYWORDS    EST.
SOURCE      Schistosoma mansoni.
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 234)
  AUTHORS   Franco,G.R. and Pena,S.D.J.
  TITLE     Franco,G.R. and Pena,S.D.J., Unpublished
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Franco G.R. and Pena S.D.J.
            Laboratorio de Genetica-Bioquimica, Departamento de Bioquimicae
            Imunologia
            Instituto de Ciencias Biologicas, Universidade Federal de Minas
            Gerais
            Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
            Tel: (5531)4415611
            Fax: (5531)4415409
            Email: gfranco@mono.icb.ufmg.br
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .234
                     /organism="Schistosoma mansoni"
                     /strain="NMRI"
                     /db_xref="taxon:6183"
                     /clone="SMPBE73"
                     /clone_lib="Schistosoma mansoni, adult worm, Gloria
                     Franco"
                     /lab_host="DH10B, JM109"
                     /note="Vector: BA vector; Site_1: NotI; Site_2: HindIII;
                     Total cellular RNA from male and female adult worms was
                     extracted  according to a modification (Puissant, C. and
                     Houdebine, L. M.  BioFeedback 8, 148-149, 1990) of the
                     Guanidine Thiocyanate  procedure (Chomczynski, P. and
                     Sacchi, N. Anal. Biochem. 162, 156- 159, 1987). Poly (A)+
                     RNA was purified by oligo dT column and cDNA  was
                     synthesized as described previously (Adams, M. D. et al.
                     Nature  Genet. 4, 373-389, 1993). cDNA was ligated to a
```

two fold molar excess of a NotI/HindIII digested plasmid DNA (lafmid BA vector, a phagemid derived from pEMBL, Adams, M. D. et al. Nature Genet. 4, 373-389, 1993)) and electroporated into E. coli strain DH10B (BRL). The library was amplified and further selected for clones containing long inserts (>500 bp) by purification of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel, containing the smear of the library and electroporation into DH10B cells. "

BASE COUNT 49 a 84 c 66 g 33 t 2 others
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 234;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaa 17
||||||||||||||||
Db 64 TACGGCGTTTCGATGAA 48

RESULT 7
T24127/c
LOCUS T24127 579 bp mRNA linear EST 27-FEB-1995
DEFINITION SMEST0325 Schistosoma mansoni, adult worm, Gloria Franco Schistosoma mansoni cDNA clone SMPBC65 3', mRNA sequence.
ACCESSION T24127
VERSION T24127.1 GI:529730
KEYWORDS EST.
SOURCE Schistosoma mansoni.
ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE 1 (bases 1 to 579)
AUTHORS Franco,G.R., Adams,M.D., Soares,M.B., Simpson,A.J.G., Venter,J.C. and Pena,S.D.J.
TITLE Identification of new Schistosoma mansoni genes by the EST strategy using a directional cDNA library
JOURNAL Gene 152, 141-147 (1995)
MEDLINE 95137379
COMMENT Contact: Franco G.R. and Pena S.D.J.
Laboratorio de Genetica-Bioquimica, Departamento de Bioquimicae Imunologia
Instituto de Ciencias Biologicas, Universidade Federal de Minas Gerais
Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
Tel: (5531)4415611
Fax: (5531)4415409
Email: gfranco@mono.icb.ufmg.br
Seq primer: M13 Forward.
FEATURES Location/Qualifiers
source 1. .579
/organism="Schistosoma mansoni"
/strain="NMRI"
/db_xref="taxon:6183"
/clone="SMPBC65"
/clone_lib="Schistosoma mansoni, adult worm, Gloria Franco"
/lab_host="DH10B, JM109"
/note="Vector: BA vector; Site_1: NotI; Site_2: HindIII; Total cellular RNA from male and female adult worms was extracted according to a modification (Puissant, C. and Houdebine, L. M. BioFeedback 8, 148-149, 1990) of the Guanidine Thiocyanate procedure (Chomczynski, P. and Sacchi, N. Anal. Biochem. 162, 156- 159, 1987). Poly (A)+ RNA was purified by oligo dT column and cDNA was synthesized as described previously (Adams, M. D. et al. Nature Genet. 4, 373-389, 1993). cDNA was ligated to a two fold molar excess of a NotI/HindIII digested plasmid DNA (lafmid BA vector, a phagemid derived from pEMBL, Adams, M. D. et al. Nature Genet. 4, 373-389, 1993)) and electroporated into E. coli strain DH10B (BRL). The library was amplified and further selected for clones containing long inserts (>500 bp) by purification of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel, containing the smear of the library and electroporation into DH10B cells. "

BASE COUNT 102 a 206 c 179 g 88 t 4 others
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaa 17
||||||||||||||||
Db 75 TACGGCGTTTCGATGAA 59

RESULT 8
AA734164
LOCUS AA734164 277 bp mRNA linear EST 07-JAN-1998
DEFINITION vs19g12.r1 Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone IMAGE:1138726 5' similar to gb:X80699 M.musculus L26 mRNA (MOUSE);, mRNA sequence.
ACCESSION AA734164
VERSION AA734164.1 GI:2755831
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 277)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:619998
Trace considered overall poor quality
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .277
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:1138726"
/clone_lib="Barstead mouse irradiated colon MPLRB7"
/dev_stage="8 weeks"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; Tissue obtained from 8 week old mouse. Colon was harvested 72 hours after irradiation with 1400 Gys. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'TGTTACGAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead. "

BASE COUNT 64 a 59 c 92 g 62 t
ORIGIN

```
  Query Match            84.0%;  Score 16.8;  DB 9;  Length 277;
  Best Local Similarity  90.0%;  Pred. No. 1.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          |||||| |||||||| ||||
Db     47 TACGGCATTTCGATGCACCC 66


RESULT  9
BF252921/c
LOCUS       BF252921                576 bp    mRNA    linear   EST 15-NOV-2001
DEFINITION  EST420184 Coccidioides immitis spherule cDNA library Coccidioides
            immitis cDNA clone CIABC49 5' sequence, mRNA sequence.
ACCESSION   BF252921
VERSION     BF252921.1  GI:16933064
KEYWORDS    EST.
SOURCE      Coccidioides immitis.
  ORGANISM  Coccidioides immitis
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE   1  (bases 1 to 576)
  AUTHORS   Gardner,M.J. and Kirkland,T.
  TITLE     Generation of ESTs from Coccidioides immitis spherule cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Malcolm J. Gardner
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org.
FEATURES             Location/Qualifiers
     source          1. .576
                     /organism="Coccidioides immitis"
                     /db_xref="taxon:5501"
                     /clone="CIABC49"
                     /clone_lib="Coccidioides immitis spherule cDNA library"
                     /dev_stage="spherule"
                     /lab_host="SOLR"
                     /note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2:
                     Xho1"
BASE COUNT      113 a    186 c    176 g    101 t
ORIGIN


  Query Match            82.0%;  Score 16.4;  DB 10;  Length 576;
  Best Local Similarity  94.4%;  Pred. No. 2.7e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 cggcgtttcgatgaaccc 20
          |||||| ||||||||||
Db    241 CGGCGTGTCGATGAACCC 224


RESULT  10
BE896357
LOCUS       BE896357                624 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601439015F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924266 5',
            mRNA sequence.
ACCESSION   BE896357
VERSION     BE896357.1  GI:10360678
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 624)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9761  row: m  column: 03
            High quality sequence start: 2
            High quality sequence stop: 403.
FEATURES             Location/Qualifiers
     source          1. .624
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3924266"
                     /clone_lib="NIH_MGC_72"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."
BASE COUNT      155 a    209 c    150 g    110 t
ORIGIN


  Query Match            82.0%;  Score 16.4;  DB 10;  Length 624;
  Best Local Similarity  94.4%;  Pred. No. 2.8e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 cggcgtttcgatgaaccc 20
          | ||||||||||||||||
Db    580 CCGCGTTTCGATGAACCC 597


RESULT  11
BH615799
LOCUS       BH615799                631 bp    DNA     linear   GSS 28-JAN-2002
DEFINITION  BMBAC304F01SP6_PSU Brugia malayi Genomic Bac Library 3 Brugia
            malayi genomic, DNA sequence.
ACCESSION   BH615799
VERSION     BH615799.1  GI:18380487
KEYWORDS    GSS.
SOURCE      Brugia malayi.
  ORGANISM  Brugia malayi
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Brugia.
REFERENCE   1  (bases 1 to 631)
  AUTHORS   Whitton,C., Daub,J., Ware,J., Quail,M., Hall,N., Barrell,B., Foster
            ,J., Guiliano,D., Slatko,B. and Blaxter,M.
  TITLE     Genome survey sequences from the human parasitic nematode Brugia
            malayi
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Blaxter ML
            Institute of Cell, Animal and Population Biology
            University of Edinburgh
            Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
            3JT, UK
            Tel: +44 131 650 6760
            Fax: +44 131 670 5450
            Email: mark.blaxter@ed.ac.uk
            Sequenced from the Brugia malayi BAC library constructed by Claire
            Whitton and Dr Mike Quail. The sequence was generated by The
            Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in
            collaboration with Mark Blaxter, ICAPB, University of Edinburgh,
            Edinburgh, UK.
            Seq primer: SP6 (ATTTAGGTGACACTATAG)
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .631
                     /organism="Brugia malayi"
```

```
                     /strain="TRS"
                     /db_xref="taxon:6279"
                     /clone_lib="Brugia malayi Genomic Bac Library 3"
                     /sex="Mixed (male and female)"
                     /tissue_type="whole parasite"
                     /dev_stage="microfilaria (L1)"
                     /note="Vector: pBACe3.6; Site_1: BamH I; Brugia malayi
                     genomic DNA was partially cleaved with Sau3A I and size
                     fractionated. 7,392 clones were generated with mean insert
                     size ~48 kbp. The library was constructed by Claire
                     Whitton, Blaxter Nematode Genetics Lab, University of
                     Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing
                     Unit, The Sanger Centre, Cambridge, UK."
BASE COUNT      196 a     94 c    142 g    199 t
ORIGIN


  Query Match             82.0%;  Score 16.4;  DB 12;  Length 631;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 acggcgtttcgatgaacc 19
          |||||||||||||| ||
Db    606 ACGGCGTTTCGATGATCC 623


RESULT  12
AG141490/c
LOCUS       AG141490                961 bp    DNA     linear   GSS 08-JAN-2002
DEFINITION  Pan troglodytes DNA, clone: RP43-001J13.TJ, genomic survey
            sequence.
ACCESSION   AG141490
VERSION     AG141490.1  GI:16671168
KEYWORDS    GSS; GSS (genome survey sequence).
SOURCE      Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
            Male BAC Library clone:RP43-001J13.TJ.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (sites)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library RPCI-43
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 961)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
            end was generated during the R&D process and may have higher chance
            of clone tracking errors.
             PRIMERS
                Sequencing: TJ
             LIBRARY
                Vector    : pBACe3.6
                R.Site 1  : EcoRI
                R.Site 2  : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .961
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /clone="RP43-001J13.TJ"
                     /sex="male"
                     /cell_type="lymphocytes"
                     /clone_lib="RPCI-43 Chimpanzee Male BAC Library"
BASE COUNT      255 a    299 c    145 g    252 t     10 others
ORIGIN
```

```
  Query Match             82.0%;  Score 16.4;  DB 12;  Length 961;
  Best Local Similarity   94.4%;  Pred. No. 3.1e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 acggcgtttcgatgaacc 19
          |||||||| |||||||||
Db    746 ACGGCGTTACGATGAACC 729


RESULT  13
AW064407/c
LOCUS       AW064407                213 bp    mRNA    linear   EST 07-DEC-2000
DEFINITION  SP0996 KRIBB Human CD4 intrathymic T-cell cDNA library Homo sapiens
            cDNA 3', mRNA sequence.
ACCESSION   AW064407
VERSION     AW064407.1  GI:8888344
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 213)
  AUTHORS   Goh,S.-H., Park,J.-H., Lee,Y.J., Lee,H.G., Yoo,H.-S., Lee,I.-C.,
            Park,J.-H., Kim,Y.-S. and Lee,C.-C.
  TITLE     Gene expression profile and identification of differentially
            expressed transcripts during human intrathymic T-cell development
            by cDNA sequencing analysis
  JOURNAL   Genomics 70 (1), 1-18 (2000)
  MEDLINE   20541704
COMMENT     Contact: Sung-Ho Goh
            Genome Center
            Korea Research Institute of Bioscience and Biotechnology
            Oun-dong 52, Yu Sung-Gu, Daejon 305-333, Republic of Korea
            Tel: 82-42-860-4473
            Fax: 82-42-860-4479
            Email: gohsh@mail.kribb.re.kr
            Seq primer: T7
            High quality sequence stop: 213
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .213
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="KRIBB Human CD4 intrathymic T-cell cDNA
                     library"
                     /tissue_type="Thymus"
                     /cell_type="Intrathymic T-cell"
                     /dev_stage="CD3+4+8- single positive stage"
                     /note="Vector: pGEM-T; cDNA was made from total
                     cytoplasmic RNA of sorted human intrathymic CD3+4+8-
                     T-cell, adaptor ligated, amplified with PCR, and cloned
                     into pGEM-T vector."
BASE COUNT       41 a     59 c     72 g     40 t      1 others
ORIGIN


  Query Match             79.0%;  Score 15.8;  DB 9;  Length 213;
  Best Local Similarity   89.5%;  Pred. No. 4.3e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 acggcgtttcgatgaaccc 20
          |||||| || |||||||||
Db     43 ACGGCGGTTTGATGAACCC 25


RESULT  14
AI496312
LOCUS       AI496312                436 bp    mRNA    linear   EST 30-NOV-2001
DEFINITION  sb05b08.y1 Gm-c1004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
            Gm-c1004-7888 5' similar to TR:Q92388 Q92388 CRG1 GENE. ;, mRNA
            sequence.
ACCESSION   AI496312
```

```
VERSION     AI496312.1  GI:4397315
KEYWORDS    EST.
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 436)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available through: ResGen, Invitrogen Corp. 2130
            South Memorial Parkway Huntsville, AL 35801 For further information
            call: (800)-533-4363 or contact via email: ccu@resgen.com
            Seq primer: -40RP from Gibco
            High quality sequence stop: 386
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .436
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
                     /clone="GENOME SYSTEMS CLONE ID: Gm-c1004-7888"
                     /clone_lib="Gm-c1004"
                     /tissue_type="root"
                     /lab_host="XL10-Gold"
                     /note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
                     XhoI; Root cDNA. The mRNA was isolated from entire roots
                     of 8 day old 'Williams' seedlings which were propagated on
                     paper towels with distilled water. Stratagene's  cDNA
                     Synthesis Kit (catalog #200401) was used to synthesize the
                     cDNA. First- strand synthesis was performed with 5-methyl
                     dCTP, hence the ligated cDNA is hemimethylated.
                     Stratagene's first-strand synthesis primer was used
                     [GAGAGAGAGAGAGAGAGAACTAGTCTCGAG(T)-18]. After
                     second-strand synthesis, the cDNA ends were 'polished'
                     with clone Pfu DNA polymerase, ligated to EcoRI adapters,
                     and phosphorylated. The XhoI site within the first-strand
                     synthesis primer was restricted by digestion with XhoI;
                     all XhoI sites in the  cDNA would be protected by their
                     hemimethylated status. The cDNA constructs were
                     size-fractionated with a 500bp cutoff, using GibcoBRL Life
                     Technologies' cDNA Size Fractionation column. The column
                     eluent was then ligated into  Stratagene's pBluescript II
                     XR Predigested vector (pBluescript II SK(+) that had been
                     digested with EcoRI and XhoI, and phosphorylated). Both
                     the white  and blue colonies appear to contain recombinant
                     plasmids with cDNA inserts. Blue colonies 9n=15) have been
                     sequenced, and possess putative cDNA inserts. This library
                     was constructed by Dr. Paul Keim & Virginia H. Coryell,
                     Department of Biology, Box5640, Northern Arizona
                     University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr.
                     Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax:
                     520-523-7500, email: paul.keim@nau.edu,
                     virginia.coryell@nau.edu"
BASE COUNT       90 a    174 c     96 g     76 t
ORIGIN
```

```
  Query Match             79.0%;  Score 15.8;  DB 9;  Length 436;
  Best Local Similarity   89.5%;  Pred. No. 5.3e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 acggcgtttcgatgaaccc 20
           ||| ||| ||||||||||||
Db     185 ACGCCGTCTCGATGAACCC 203


RESULT 15
CNS01K68/c
LOCUS       CNS01K68                582 bp    DNA     linear   GSS 12-JUN-2001
DEFINITION  Anopheles gambiae GSS SP6 end of clone 16E18 of NotreDame1 library
            from strain PEST of Anopheles gambiae (African malaria mosquito),
            genomic survey sequence.
ACCESSION   AL147937
VERSION     AL147937.1  GI:7006083
KEYWORDS    GSS.
SOURCE      African malaria mosquito.
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
            Culicoidea; Anopheles.
REFERENCE   1  (bases 1 to 582)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
REFERENCE   2  (bases 1 to 582)
  AUTHORS   Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
            Roux, Paris 75015, France
COMMENT     This clone is from an A. gambiae BAC library provided by F.H.
            Collins and sequenced by Genoscope in collaboration with the
            Laboratory of Biochem. and Biol. Molec. of Insects, Institut
            Pasteur.
FEATURES             Location/Qualifiers
     source          1. .582
                     /organism="Anopheles gambiae"
                     /strain="PEST"
                     /db_xref="taxon:7165"
                     /clone="16E18"
                     /clone_lib="NotreDame1"
                     /note="end : SP6"
BASE COUNT      160 a    124 c    136 g    153 t      9 others
ORIGIN
```

```
  Query Match             79.0%;  Score 15.8;  DB 12;  Length 582;
  Best Local Similarity   89.5%;  Pred. No. 5.7e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 acggcgtttcgatgaaccc 20
           |||||||||||||| | ||
Db     320 ACGGCGTTTCGATGTAGCC 302


Search completed: August  7, 2002, 21:15:21
Job time: 22891 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 22:04:01 ; Search time 568.44 Seconds
(without alignments)
60.408 Million cell updates/sec

Title: US-09-786-105-4
Perfect score: 20
Sequence: 1 tacggcgtttcgatgaaccc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*
1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
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6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
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15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
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21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		20	100.0	20	21	AAA49824	Mycobacterium tube
2		20	100.0	20	21	AAA49826	Mycobacterium tube
c 3		20	100.0	432	14	AAQ61457	M.tuberculosis rpo
c 4		20	100.0	480	21	AAA49863	Mycobacterium tube
c 5		20	100.0	620	17	AAT29126	rpoB gene fragment
c 6		20	100.0	620	17	AAT29124	rpoB gene fragment
c 7		20	100.0	620	17	AAT29125	rpoB gene fragment
c 8		20	100.0	970	17	AAT09676	Mycobacterium tube
c 9		20	100.0	3519	22	AAH51976	Mycobacterium tube
c 10		20	100.0	3534	22	AAH02079	Mycobacterium tube
c 11		20	100.0	3853	21	AAA74651	Mycobacterium tube
c 12		20	100.0	3853	21	AAA89994	M. tuberculosis rp
13		19	95.0	19	17	AAT12096	M. tuberculosis rp
c 14		18.4	92.0	3447	14	AAQ51532	M.leprae rpoB gene
c 15		16.8	84.0	3474	23	AAS51357	Enterococcus faeca
c 16		16.8	84.0	3624	23	AAS52892	Enterococcus faeca
17		16.8	84.0	9179	20	AAX13246	Enterococcus faeca
c 18		15.4	77.0	612	22	AAF71082	C. glutamicum SRT
c 19		15.4	77.0	1344	22	AAH68297	C glutamicum codin
20		15.4	77.0	6275	24	ABL32551	Human immune syste
c 21		15.4	77.0	309400	22	AAH68534	C glutamicum codin
c 22		15.2	76.0	1446	21	AAC42071	Arabidopsis thalia
23		15.2	76.0	2853	23	ABL12631	Drosophila melanog
24		15.2	76.0	3276	23	ABL02493	Drosophila melanog
25		15.2	76.0	4505	21	AAA15009	Nucleotide sequenc
c 26		15.2	76.0	5574	23	ABL02492	Drosophila melanog
c 27		15.2	76.0	7243	23	ABL02521	Drosophila melanog
c 28		15.2	76.0	8193	23	ABL12630	Drosophila melanog
c 29		15.2	76.0	21748	23	ABL02520	Drosophila melanog
c 30		15.2	76.0	27426	23	AAS59541	Propionibacterium
31		15.2	76.0	4403765	22	AAI99683	Mycobacterium tube
32		15	75.0	27	17	AAT09670	Mycobacterium tube
33		14.8	74.0	822	23	AAS54258	Pseudomonas aerugi
c 34		14.8	74.0	894	23	AAS51512	Pseudomonas aerugi
35		14.8	74.0	1167	22	AAF81355	Quorum sensing con
36		14.8	74.0	2176	15	AAQ57017	PKC nu. Bos tauru
c 37		14.4	72.0	1014	22	AAH65487	C glutamicum codin
c 38		14.4	72.0	1086	23	AAS93170	DNA encoding novel
c 39		14.4	72.0	1086	23	AAS93247	DNA encoding novel
40		14.4	72.0	1578	21	AAC48875	Arabidopsis thalia
41		14.4	72.0	1579	21	AAC40928	Arabidopsis thalia
c 42		14.4	72.0	2660	23	ABL10327	Drosophila melanog
43		14.4	72.0	3342	23	ABL23542	Drosophila melanog
44		14.4	72.0	3366	23	ABL17225	Drosophila melanog
45		14.4	72.0	3632	23	ABL13365	Drosophila melanog

ALIGNMENTS

RESULT 1
AAA49824
ID AAA49824 standard; DNA; 20 BP.
XX
AC AAA49824;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene amplification primer rpoB-R.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX

PS Claim 4; Page 4; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene amplification primer rpoB-R (bp
CC 2611-2592). It is used with the forward primer given in AAA49823
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 1 tacggcgtttcgatgaaccc 20

RESULT 2
AAA49826
ID AAA49826 standard; DNA; 20 BP.
XX
AC AAA49826;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-3s.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene sequencing primer rpoB-3s (bp
CC 2611-2592). It is used with the forward primer given in AAA49825 and
CC with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 1 tacggcgtttcgatgaaccc 20

RESULT 3
AAQ61457/c
ID AAQ61457 standard; DNA; 432 BP.
XX
AC AAQ61457;
XX
DT 17-MAY-1994 (first entry)
XX
DE M.tuberculosis rpoB gene fragment.
XX
KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KW mutant; ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9322454-A.
XX
PD 11-NOV-1993.
XX
PF 30-APR-1993; 93WO-EP01063.
XX
PR 17-SEP-1992; 92FR-0011098.
PR 30-APR-1992; 92US-0875940.
PR 14-AUG-1992; 92US-0929206.
PR 16-APR-1993; 93FR-0004545.
XX
PA (ASSI-) ASSISTANCE PUBLIQUE.
PA (INSP) INST PASTEUR.
PA (MEDI-) MEDICAL RES COUNCIL.
PA (UYBE-) UNIV BERNE.
PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
PI Young D, Zhang Y;
XX
DR WPI; 1993-368812/46.
DR P-PSDB; AAR51372.
XX

PT Rapid detection of antibiotic resistance in Mycobacteria - esp.
PT isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in katG, rpoB or rpsL genes
XX
PS Example 2; Fig 13; 97pp; English.
XX
CC PCR amplification was used to obtain rpoB genes from rifampicin-
CC resistant Mycobacterium leprae strains. A comparison with the
CC sequence of the rpoB gene from sensitive strains (AAQ51532) revealed
CC mutations in the region encoding amino acids 400-450. The corresp.
CC region was isolated from M.tuberculosis (AAQ61457). A common
CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
SQ Sequence 432 BP; 78 A; 139 C; 148 G; 67 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 428 TACGGCGTTTCGATGAACCC 409

RESULT 4
AAA49863/c
ID AAA49863 standard; DNA; 480 BP.
XX
AC AAA49863;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene (rifampin resistance).
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; ss.
XX
OS Mycobacterium tuberculosis.
XX
FH Key Location/Qualifiers
FT primer_bind complement(41..60)
FT /*tag= a
FT /note= "primer of AAA49823"
FT primer_bind 372..391
FT /*tag= b
FT /note= "primer of AAA49824"
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Disclosure; Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene (bp2161-2640). Amplification and
CC cycle sequencing primers (see AAA49823-62) are used for the detection
CC and analysis of antibiotic resistance-associated mutations in
CC defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 451 TACGGCGTTTCGATGAACCC 432

RESULT 5
AAT29126/c
ID AAT29126 standard; DNA; 620 BP.
XX
AC AAT29126;
XX
DT 02-DEC-1996 (first entry)
XX
DE rpoB gene fragment (mutant) from Mycobacterium tuberculosis.
XX
KW p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus;
KW Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
KW Staphylococcus; identification; detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US14673.
XX
PR 30-AUG-1995; 95US-0520946.
PR 09-NOV-1994; 94US-0337164.
PR 09-MAR-1995; 95US-0402601.
PR 07-JUN-1995; 95US-0484956.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM;
XX
DR WPI; 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
PS Example 33; Page 306; 433pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene; for
CC identifying strains of microorganisms, especially bacteria selected
CC from the the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the Mycobacterium tuberculosis rpoB gene, which, when
CC mutated is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451Y and S456L mutations. The amplified
CC fragments are given in AAT29124 (Wild type) and AAT29125-26
CC (mutant sequences).
XX
SQ Sequence 620 BP; 103 A; 201 C; 214 G; 102 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
AAT29124/c
ID AAT29124 standard; DNA; 620 BP.
XX
AC AAT29124;
XX
DT 02-DEC-1996 (first entry)
XX
DE rpoB gene fragment from Mycobacterium tuberculosis.
XX
KW p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus;
KW Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
KW Staphylococcus; identification; detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US14673.
XX
PR 30-AUG-1995; 95US-0520946.
PR 09-NOV-1994; 94US-0337164.
PR 09-MAR-1995; 95US-0402601.
PR 07-JUN-1995; 95US-0484956.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM;
XX
DR WPI; 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
PS Example 33; Page 305; 433pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene; for
CC identifying strains of microorganisms, especially bacteria selected
CC from the the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the Mycobacterium tuberculosis rpoB gene, which, when
CC mutated is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451Y and S456L mutations. The amplified
CC fragments are given in AAT29124 (Wild type) and AAT29125-26
CC (mutant sequences).
XX
SQ Sequence 620 BP; 103 A; 202 C; 214 G; 101 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 7
AAT29125/c
ID AAT29125 standard; DNA; 620 BP.
XX
AC AAT29125;
XX
DT 02-DEC-1996 (first entry)
XX
DE rpoB gene fragment (mutant) from Mycobacterium tuberculosis.
XX
KW p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus;
KW Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
KW Staphylococcus; identification; detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US14673.
XX
PR 30-AUG-1995; 95US-0520946.
PR 09-NOV-1994; 94US-0337164.
PR 09-MAR-1995; 95US-0402601.
PR 07-JUN-1995; 95US-0484956.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM;
XX
DR WPI; 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
PS Example 33; Page 305-306; 433pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

```
CC   compared to the cleavage products of reference gene sequences.  The
CC   method is used for detecting mutation in the human p53 gene; for
CC   identifying strains of microorganisms, especially bacteria selected
CC   from the the group of members of the genera Campylobacter,
CC   Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC   The method may also be used for the identification of viruses,
CC   especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC   (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC   region of the Mycobacterium tuberculosis rpoB gene, which, when
CC   mutated is associated with rifampin resistance. The 620 bp region
CC   amplified spans both the H451Y and S456L mutations.  The amplified
CC   fragments are given in AAT29124 (Wild type) and AAT29125-26
CC   (mutant sequences).
XX
SQ   Sequence 620 BP; 103 A; 201 C; 214 G; 102 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 17;  Length 620;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    296 TACGGCGTTTCGATGAACCC 277


RESULT   8
AAT09676/c
ID   AAT09676 standard; DNA; 970 BP.
XX
AC   AAT09676;
XX
DT   15-OCT-1996  (first entry)
XX
DE   Mycobacterium tuberculosis rpoB gene DNA sequence.
XX
KW   Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;
KW   polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.
XX
OS   Mycobacterium tuberculosis.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     10..27
FT                   /*tag=  a
FT                   /note= "primer FENLFF"
FT   primer_bind     226..243
FT                   /*tag=  b
FT                   /note= "primer DDIDHL"
FT   primer_bind     226..240
FT                   /*tag=  c
FT                   /note= "primer DDIDH"
FT   primer_bind     338..364
FT                   /*tag=  d
FT                   /note= "primer rpo95"
FT   primer_bind     348..373
FT                   /*tag=  e
FT                   /note= "primer rpo105"
FT   primer_bind     354..373
FT                   /*tag=  f
FT                   /note= "primer KY290"
FT   misc_feature    372..373
FT                   /*tag=  g
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    433..434
FT                   /*tag=  h
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    438
FT                   /*tag=  i
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    468..469
FT                   /*tag=  j
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    486
FT                   /*tag=  k
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    501
FT                   /*tag=  l
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    516
FT                   /*tag=  m
FT                   /note= "M. tuberculosis signature nucleotide"
FT   primer_bind     516..535
FT                   /*tag=  n
FT                   /note= "primer rpo273"
FT   misc_feature    525
FT                   /*tag=  o
FT                   /note= "M. tuberculosis signature nucleotide"
FT   primer_bind     525..541
FT                   /*tag=  p
FT                   /note= "primer KY292"
FT   primer_bind     536..562
FT                   /*tag=  q
FT                   /note= "primer rpo293"
FT   primer_bind     640..666
FT                   /*tag=  r
FT                   /note= "primer rpo397"
FT   primer_bind     952..966
FT                   /*tag=  s
FT                   /note= "primer NMQRQ-1"
FT   primer_bind     952..966
FT                   /*tag=  t
FT                   /note= "primer NMQRQ-2"
XX
PN   WO9533074-A1.
XX
PD   07-DEC-1995.
XX
PF   26-MAY-1995;   95WO-US06790.
XX
PR   26-MAY-1994;   94US-0250030.
XX
PA   (HOFF ) HOFFMANN LA ROCHE INC.
PA   (MAYO-) MAYO FOUNDATION.
XX
PI   Felmlee TA,  Hunt JM,  Persing DH,  Roberts GD,  Whelen AC;
PI   Young KKY;
XX
DR   WPI; 1996-030581/03.
XX
PT   Detection of Mycobacterium tuberculosis - by amplifying sample DNA
PT   with a primer set that targets portions of the gene encoding rpoB.
XX
PS   Disclosure; Fig.3; 54pp; English.
XX
CC   This oligonucleotide DNA primer is specific for Mycobacterium
CC   tuberculosis, and may be used to amplify a sample DNA by targeting
CC   a portion of the gene encoding rpoB.  The 1st several bases comprise a
CC   nonhybridizing tail consisting of filler bases followed by
CC   a restriction site incorporated to facilitate cloning using the
CC   amplicon at a later date, if desired.  The remaining bases hybridize
CC   to bacterial rpoB DNA.  The method provides for the detection of M.
CC   tuberculosis and the concurrent determination of its drug
CC   susceptibility, particularly to rifamycin.  The method can provide
CC   often greater than 95% sensitivity and 100% specificity.  The
CC   biological sample is a fluid or tissue sample from a human.
XX
SQ   Sequence 970 BP; 182 A; 302 C; 330 G; 156 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 17;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 0.39;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    671 TACGGCGTTTCGATGAACCC 652
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RESULT   9
AAH51976/c
ID   AAH51976 standard; DNA; 3519 BP.
XX
AC   AAH51976;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Mycobacterium tuberculosis potential drug target gene SEQ ID 30.
XX
KW   Drug target; growth; organism viability; characterisation; ds.
XX
OS   Mycobacterium tuberculosis.
XX
PN   WO200135317-A1.
XX
PD   17-MAY-2001.
XX
PF   13-NOV-2000; 2000WO-US31152.
XX
PR   12-NOV-1999;   99US-0165086.
PR   12-NOV-1999;   99US-0165124.
PR   01-FEB-2000; 2000US-0179531.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Eisenberg D,  Rotstein SH,  Marcotte EM;
XX
DR   WPI; 2001-329193/34.
DR   P-PSDB; AAG81125.
XX
PT   Identifying nucleotide or polypeptide sequence for use as drug target,
PT   involves providing algorithm that analyzes a functional relationship
PT   between nucleotide or polypeptide sequences, and comparing the
PT   sequences  -
XX
PS   Disclosure; Page 68-69; 207pp; English.
XX
CC   This invention relates to a method for identifying a nucleotide or
CC   polypeptide sequence that may be a drug target, or essential for growth
CC   or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
CC   represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
CC   tuberculosis proteins which are potential drug targets. The DNA and
CC   protein sequences are used to illustrate the method of the invention. The
CC   method involves providing an unknown nucleotide or polypeptide sequences,
CC   and comparing it to a number of sequences along with at least one
CC   algorithm capable of analysing a functional relationship between
CC   nucleotide and polypeptide sequences. The method is useful for
CC   characterising the function of nucleic acids and polypeptides that may be
CC   useful as a target for a drug or essential for the growth or viability of
CC   an organism.
XX
SQ   Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 22;  Length 3519;
  Best Local Similarity   100.0%;  Pred. No. 0.42;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db   1529 TACGGCGTTTCGATGAACCC 1510


RESULT  10
AAH02079/c
ID   AAH02079 standard; DNA; 3534 BP.
XX
AC   AAH02079;
XX
DT   24-JUL-2001  (first entry)
XX
DE   Mycobacterium tuberculosis nucleotide sequence SEQ ID NO:2072.
XX
KW   Species specific; genus specific; family specific; probe; detection;
KW   identification; algal; archaeal; bacterial; fungal; parasitical;
KW   microorganism; diagnosis; translation elongation factor Tu; toxin;
KW   translation elongation factor G; RecA recombinase; resistance;
KW   catalytic subunit of proton-translocating ATPase; antimicrobial;
KW   vaccine; primer; ds.
XX
OS   Mycobacterium tuberculosis.
XX
PN   WO200123604-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-CA01150.
XX
PR   28-SEP-1999;   99CA-2283458.
PR   19-MAY-2000; 2000CA-2307010.
XX
PA   (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI   Bergeron MG,  Boissinot M,  Huletsky A,  Menard C,  Ouellette M;
PI   Picard FJ,  Roy PH;
XX
DR   WPI; 2001-245006/25.
XX
PT   Nucleic acid sequences are used to generate universal probes and
PT   primers which can be used to identify and detect the presence of algal,
PT   archaeal, bacterial, fungal and parasitical species in a test sample -
XX
PS   Disclosure; Page 1478-1479; 1580pp; English.
XX
CC   The present invention describes a method for generating a repertory of
CC   nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC   and/or primers are derived. The method comprises amplifying the nucleic
CC   acids of determined algal, archaeal, bacterial, fungal and parasitical
CC   species with a combination of defined primer pairs. The method can be
CC   used for producing probes and/or primers for detecting one or more
CC   related microorganisms e.g. algae, archaea, bacteria, fungi and
CC   parasites, for universal detection and for specific and ubiquitous
CC   detection and identification of an algal, archaeal, bacterial, fungal
CC   and parasitical species, genus, family and group. A nucleic acid (I)
CC   obtained using the method of the invention can be used for the universal
CC   detection of any bacterium, fungus or parasite in a sample and for the
CC   detection of at least one antimicrobial agent resistance gene or at
CC   least one toxin gene. hexA nucleic acids are used for the specific and
CC   ubiquitous detection and for identification of Streptococcus pneumoniae.
CC   (I) can be used to design a therapeutic agent which is effective against
CC   microorganisms. Microbial species or genus or family or phylum or group
CC   which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC   Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC   Mycobacteriaceae family, Pseudomonads group, Streptococcus sp.,
CC   Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests
CC   provides faster results than substrate specificity tests as results can
CC   be determined in an hour and improved accuracy is also achieved.
CC   AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
CC   which are given in the exemplification of the present invention.
XX
SQ   Sequence 3534 BP; 679 A; 1081 C; 1188 G; 586 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 22;  Length 3534;
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Qy      1 tacggcgtttcgatgaaccc 20
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Db   1547 TACGGCGTTTCGATGAACCC 1528


RESULT  11
```

```
AAA74651/c
ID   AAA74651 standard; DNA; 3853 BP.
XX
AC   AAA74651;
XX
DT   06-DEC-2000  (first entry)
XX
DE   Mycobacterium tuberculosis rpoB gene.
XX
KW   Mycobacterium tuberculosis; rpoB; RNA polymerase beta subunit;
KW   rifampin resistance; mutation detection; ds.
XX
OS   Mycobacterium tuberculosis.
XX
PN   WO200043546-A2.
XX
PD   27-JUL-2000.
XX
PF   20-DEC-1999;   99WO-US30377.
XX
PR   19-JAN-1999;   99US-0233996.
XX
PA   (DADE-) DADE BEHRING INC.
XX
PI   Liu YP,  Kurn N;
XX
DR   WPI; 2000-524243/47.
XX
PT   Method for detecting drug resistance in a strain of an organism,
PT   particularly for detecting rifampin resistance in Mycobacterium
PT   tuberculosis  -
XX
PS   Example 1; Fig 4; 86pp; English.
XX
CC   The present sequence is the rpoB gene from Mycobacterium tuberculosis.
CC   Rifampin resistance is largely associated with point mutations
CC   localised in a small core region of 81 base pairs in the rpoB gene, which
CC   encodes the RNA polymerase beta subunit. To detect a mutation, a complex
CC   is formed comprising a first sequence representing the predetermined
CC   region of the gene of the organism and a second sequence representing the
CC   corresponding region of the gene of the wild type organism in double
CC   stranded form. Each member of at least one pair of non-complementary
CC   strands within the complex has a label. The association of the labels in
CC   the complex is related to the presence of the mutation. The presence of
CC   the mutation is related to the drug resistance of the strain.
XX
SQ   Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 21;  Length 3853;
  Best Local Similarity   100.0%;  Pred. No. 0.42;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db   2122 TACGGCGTTTCGATGAACCC 2103


RESULT  12
AAA89994/c
ID   AAA89994 standard; DNA; 3853 BP.
XX
AC   AAA89994;
XX
DT   18-DEC-2000  (first entry)
XX
DE   M. tuberculosis rpoB gene encoding RNA polymerase beta subunit.
XX
KW   Drug resistance; rifampin; rifampicin; pyrazinamide; rpoB;
KW   RNA polymerase beta subunit; ds.
XX
OS   Mycobacterium tuberculosis.
XX
PN   WO200043545-A2.
XX
PD   27-JUL-2000.
XX
PF   14-DEC-1999;   99WO-US29517.
XX
PR   19-JAN-1999;   99US-0233996.
PR   22-APR-1999;   99US-0296894.
XX
PA   (DADE-) DADE BEHRING INC.
XX
PI   Liu YP,  Kurn N;
XX
DR   WPI; 2000-499235/44.
XX
PT   Detecting resistance of drugs such as rifampicin in strains of
PT   Mycobacterium, comprising detecting mutations in a gene and relating
PT   them to drug resistance -
XX
PS   Example 1; Fig 4; 91pp; English.
XX
CC   This invention relates to a method for detecting drug resistance in a
CC   strain of an organism. The method comprises detecting the presence of at
CC   least 1 mutation in a first sequence and relating the presence of the
CC   mutation to drug resistance. Included in the invention are a kit for
CC   carrying out the method and a method for detecting the presence of a
CC   difference between two related nucleic acid sequences in an organism. The
CC   methods are useful for detecting resistance to drugs such rifampin and
CC   pyrazinamide in Mycobacterium. The present sequence represents the
CC   Mycobacterium tuberculosis rpoB gene (which encodes the RNA polymerase
CC   beta subunit). The sequence is used in an example of the method of the
CC   invention for the detection of rifampin resistance in M. tuberculosis.
XX
SQ   Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 21;  Length 3853;
  Best Local Similarity   100.0%;  Pred. No. 0.42;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db   2122 TACGGCGTTTCGATGAACCC 2103


RESULT  13
AAT12096
ID   AAT12096 standard; DNA; 19 BP.
XX
AC   AAT12096;
XX
DT   10-JUL-1996  (first entry)
XX
DE   M. tuberculosis rpoB gene fragment amplification primer P6.
XX
KW   Antibiotic; resistance; spectrum; gene; mycobacterium;
KW   determination; amplification; tuberculosis; rpoB; fragment;
KW   primer; differential; hybridisation; pattern; rifampicin;
KW   rifabutin; species identification; ss.
XX
OS   Synthetic.
XX
PN   WO9533851-A2.
XX
PD   14-DEC-1995.
XX
PF   09-JUN-1995;   95WO-EP02230.
XX
PR   09-JUN-1994;   94EP-0870093.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   De Beenhouwer H,  Jannes G,  Machtelinckx L,  Portaels F;
```

PI Rossau R;
XX
DR WPI; 1996-040250/04.
XX
PT Probes and primers for determn. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene
XX
PS Claim 22; Page 39; 69pp; English.
XX
CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT12091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrids formed and
CC inferring the ARS, and opt. the spp., from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampicin and/or rifabutin resistance in M. leprae
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determn.
CC of ARS and spp. identity.
XX
SQ Sequence 19 BP; 4 A; 5 C; 5 G; 5 T; 0 other;

Query Match 95.0%; Score 19; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaacc 19
||||||||||||||||||||
Db 1 tacggcgtttcgatgaacc 19

RESULT 14
AAQ51532/c
ID AAQ51532 standard; DNA; 3447 BP.
XX
AC AAQ51532;
XX
DT 17-MAY-1994 (first entry)
XX
DE M.leprae rpoB gene.
XX
KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KW mutant; ss.
XX
OS Mycobacterium leprae.
XX
FH Key Location/Qualifiers
FT CDS 1..3447
FT /*tag= a
FT /note= "rifampicin-sensitive; in resistant
FT strains the Ser codon (TCG at
FT nucleotides 1273-1275) is often mutated
FT to a Phe, Met or esp. Leu codon"
XX
PN WO9322454-A.
XX
PD 11-NOV-1993.
XX
PF 30-APR-1993; 93WO-EP01063.
XX
PR 17-SEP-1992; 92FR-0011098.
PR 30-APR-1992; 92US-0875940.
PR 14-AUG-1992; 92US-0929206.
PR 16-APR-1993; 93FR-0004545.
XX
PA (ASSI-) ASSISTANCE PUBLIQUE.
PA (INSP) INST PASTEUR.
PA (MEDI-) MEDICAL RES COUNCIL.
PA (UYBE-) UNIV BERNE.
PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
PI Young D, Zhang Y;
XX
DR WPI; 1993-368812/46.
DR P-PSDB; AAR43671.
XX
PT Rapid detection of antibiotic resistance in Mycobacteria - esp.
PT isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in katG, rpoB or rpsL genes
XX
PS Example 2; Fig 12; 97pp; English.
XX
CC PCR amplification was used to obtain rpoB genes from rifampicin-
CC resistant Mycobacterium leprae strains. A comparison with the
CC sequence of the rpoB gene from sensitive strains (AAQ51532) revealed
CC mutations in the region encoding amino acids 400-450. A common
CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
SQ Sequence 3447 BP; 687 A; 965 C; 1139 G; 656 T; 0 other;

Query Match 92.0%; Score 18.4; DB 14; Length 3447;
Best Local Similarity 95.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||| ||||||||||||||
Db 1454 TACGGTGTTTCGATGAACCC 1435

RESULT 15
AAS51357/c
ID AAS51357 standard; DNA; 3474 BP.
XX
AC AAS51357;
XX
DT 13-FEB-2002 (first entry)
XX
DE Enterococcus faecalis DNA for cellular proliferation protein #134.
XX
KW Antisense; ds; prokaryotic cellular proliferation gene;
KW antibiotic; antibacterial; drug design.
XX
OS Enterococcus faecalis.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR P-PSDB; AAU33498.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
PS Claim 27; Seq ID No 3939; 511pp; English.

XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence encodes an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 3474 BP; 1074 A; 691 C; 776 G; 933 T; 0 other;

Query Match 84.0%; Score 16.8; DB 23; Length 3474;
Best Local Similarity 90.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
|| ||||||||||||| ||
Db 1652 TAAGGCGTTTCGATGAAACC 1633

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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:51:38 ; Search time 2167.9 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: gb_pl:*
9: gb_pr:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
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23: em_pat:*
24: em_ph:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	20	100.0	432	1	MSGRIFRNAP	L05910 Mycobacteri
c 2	20	100.0	432	6	AR067448	AR067448 Sequence
c 3	20	100.0	620	6	AR062056	AR062056 Sequence
c 4	20	100.0	620	6	AR062057	AR062057 Sequence
c 5	20	100.0	620	6	AR062058	AR062058 Sequence
6	20	100.0	620	6	AR062059	AR062059 Sequence
7	20	100.0	620	6	AR062060	AR062060 Sequence
8	20	100.0	620	6	AR062061	AR062061 Sequence
c 9	20	100.0	705	1	AF060353	AF060353 Mycobacte
c 10	20	100.0	706	6	AR149128	AR149128 Sequence
c 11	20	100.0	970	6	I50706	I50706 Sequence 1
c 12	20	100.0	3534	6	AX111339	AX111339 Sequence
c 13	20	100.0	3853	1	MTU12205	U12205 Mycobacteri
c 14	20	100.0	5084	1	MSGRPOB	L27989 Mycobacteri
c 15	20	100.0	19352	1	AE006964	AE006964 Mycobacte
c 16	20	100.0	19770	1	MTCI376	Z95972 Mycobacteri
c 17	18.4	92.0	626	1	AF060295	AF060295 Mycobacte
c 18	18.4	92.0	703	1	AF060349	AF060349 Mycobacte
c 19	18.4	92.0	705	1	AF060279	AF060279 Mycobacte
c 20	18.4	92.0	705	1	AF060290	AF060290 Mycobacte
c 21	18.4	92.0	705	1	AF060293	AF060293 Mycobacte
c 22	18.4	92.0	705	1	AF060297	AF060297 Mycobacte
c 23	18.4	92.0	705	1	AF060299	AF060299 Mycobacte
c 24	18.4	92.0	705	1	AF060300	AF060300 Mycobacte
c 25	18.4	92.0	705	1	AF060325	AF060325 Mycobacte
c 26	18.4	92.0	705	1	AF060326	AF060326 Mycobacte
c 27	18.4	92.0	705	1	AF060327	AF060327 Mycobacte
c 28	18.4	92.0	705	1	AF060328	AF060328 Mycobacte
c 29	18.4	92.0	705	1	AF060329	AF060329 Mycobacte
c 30	18.4	92.0	705	1	AF060331	AF060331 Mycobacte
c 31	18.4	92.0	705	1	AF060351	AF060351 Mycobacte
c 32	18.4	92.0	705	1	AF060366	AF060366 Mycobacte
c 33	18.4	92.0	3316	1	AF172323	AF172323 Bacillus
c 34	18.4	92.0	3447	6	AR067447	AR067447 Sequence
c 35	18.4	92.0	37617	1	MLB1790G	Z14314 M.leprae ge
36	18.4	92.0	348950	1	MLEPRTN7	AL583923 Mycobacte
c 37	17.4	87.0	10909	1	AE007977	AE007977 Agrobacte
c 38	17.4	87.0	13047	1	AE009010	AE009010 Agrobacte
39	16.8	84.0	518	1	AF325874	AF325874 Staphyloc
c 40	16.8	84.0	643	1	AF060346	AF060346 Mycobacte
c 41	16.8	84.0	647	1	AF060350	AF060350 Mycobacte
c 42	16.8	84.0	652	1	AF060344	AF060344 Mycobacte
c 43	16.8	84.0	652	1	AF060364	AF060364 Mycobacte
c 44	16.8	84.0	705	1	AF060283	AF060283 Mycobacte
c 45	16.8	84.0	705	1	AF060285	AF060285 Mycobacte

ALIGNMENTS

RESULT 1
MSGRIFRNAP/c
LOCUS MSGRIFRNAP 432 bp DNA linear BCT 21-MAY-1993
DEFINITION Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin resistance gene, complete cds.
ACCESSION L05910
VERSION L05910.1 GI:149991
KEYWORDS RNA polymerase beta-subunit; rifampicin resistance.
SOURCE Mycobacterium tuberculosis (strain H37) DNA.
ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 432)
AUTHORS Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T., Colston,J., Matter,L., Schopfer,K. and Bodmer,T.
TITLE Detection of rifampicin-resistance mutation in Mycobacterium tuberculosis
JOURNAL Antimicrob. Agents Chemother. 341, 647-650 (1993)
FEATURES Location/Qualifiers
source 1. .432
/organism="Mycobacterium tuberculosis"
/strain="H37"

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                /codon_start=1
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                /protein_id="AAB59068.1"
                /db_xref="GI:149992"
                /translation="GNRRLRTVGELIQNQIRVGMSRMERVVRERMTTQDVEAITPQTL
                INIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDV
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     variation  149
                /phenotype="rifampicin resistant in association with
                mutation 234 G"
                /replace="c"
     variation  188
                /phenotype="rifampicin resistant"
                /replace="c"
     variation  191
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                mutation 203 T"
                /replace="c"
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                /replace="t"
     variation  203
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BASE COUNT      77 a    140 c    148 g     67 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 1;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    428 TACGGCGTTTCGATGAACCC 409


RESULT   2
AR067448/c
LOCUS       AR067448                 432 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 59 from patent US 5851763.
ACCESSION   AR067448
VERSION     AR067448.1  GI:5998670
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 432)
  AUTHORS   Heym,B., Cole,S., Young,D., Zhang,Y., Honore,N., Telenti,A. and
            Bodmer,T.
  TITLE     Rapid detection of antibiotic resistance in mycobacterium
            tuberculosis
  JOURNAL   Patent: US 5851763-A 59 22-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .432
                     /organism="unknown"
BASE COUNT      77 a    139 c    149 g     67 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 6;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    428 TACGGCGTTTCGATGAACCC 409


RESULT   3
AR062056/c
LOCUS       AR062056                 620 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 135 from patent US 5843669.
ACCESSION   AR062056
VERSION     AR062056.1  GI:5989747
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
  TITLE     Cleavage of nucleic acid acid using thermostable methoanococcus
            jannaschii FEN-1 endonucleases
  JOURNAL   Patent: US 5843669-A 135 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .620
                     /organism="unknown"
BASE COUNT     103 a    202 c    214 g    101 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 6;  Length 620;
  Best Local Similarity   100.0%;  Pred. No. 1.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    296 TACGGCGTTTCGATGAACCC 277


RESULT   4
AR062057/c
LOCUS       AR062057                 620 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 136 from patent US 5843669.
ACCESSION   AR062057
VERSION     AR062057.1  GI:5989748
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
  TITLE     Cleavage of nucleic acid acid using thermostable methoanococcus
```

```
          jannaschii FEN-1 endonucleases
  JOURNAL   Patent: US 5843669-A 136 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .620
                     /organism="unknown"
BASE COUNT      103 a    201 c    214 g    102 t
ORIGIN
```

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    296 TACGGCGTTTCGATGAACCC 277
```

```
RESULT   5
AR062058/c
LOCUS       AR062058                620 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 137 from patent US 5843669.
ACCESSION   AR062058
VERSION     AR062058.1  GI:5989749
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
  TITLE     Cleavage of nucleic acid acid using thermostable methoanococcus
            jannaschii FEN-1 endonucleases
  JOURNAL   Patent: US 5843669-A 137 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .620
                     /organism="unknown"
BASE COUNT      103 a    201 c    214 g    102 t
ORIGIN
```

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    296 TACGGCGTTTCGATGAACCC 277
```

```
RESULT   6
AR062059
LOCUS       AR062059                620 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 138 from patent US 5843669.
ACCESSION   AR062059
VERSION     AR062059.1  GI:5989750
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
  TITLE     Cleavage of nucleic acid acid using thermostable methoanococcus
            jannaschii FEN-1 endonucleases
  JOURNAL   Patent: US 5843669-A 138 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .620
                     /organism="unknown"
BASE COUNT      101 a    214 c    202 g    103 t
ORIGIN
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Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    325 TACGGCGTTTCGATGAACCC 344
```

```
RESULT   7
AR062060
LOCUS       AR062060                620 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 139 from patent US 5843669.
ACCESSION   AR062060
VERSION     AR062060.1  GI:5989751
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
  TITLE     Cleavage of nucleic acid acid using thermostable methoanococcus
            jannaschii FEN-1 endonucleases
  JOURNAL   Patent: US 5843669-A 139 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .620
                     /organism="unknown"
BASE COUNT      102 a    214 c    201 g    103 t
ORIGIN
```

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    325 TACGGCGTTTCGATGAACCC 344
```

```
RESULT   8
AR062061
LOCUS       AR062061                620 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 140 from patent US 5843669.
ACCESSION   AR062061
VERSION     AR062061.1  GI:5989752
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
  TITLE     Cleavage of nucleic acid acid using thermostable methoanococcus
            jannaschii FEN-1 endonucleases
  JOURNAL   Patent: US 5843669-A 140 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .620
                     /organism="unknown"
BASE COUNT      102 a    214 c    201 g    103 t
ORIGIN
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Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    325 TACGGCGTTTCGATGAACCC 344
```

```
RESULT   9
AF060353/c
LOCUS       AF060353                705 bp    DNA     linear   BCT 15-MAY-1998
DEFINITION  Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB) gene,
```

```
            partial cds.
ACCESSION   AF060353
VERSION     AF060353.1  GI:3133464
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 705)
  AUTHORS   Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
            Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
  TITLE     Simultaneous genotyping and species identification using
            hybridization pattern recognition analysis of generic mycobacterium
            DNA arrays
  JOURNAL   Genome Res. 8 (5), 435-448 (1998)
  MEDLINE   98248685
REFERENCE   2  (bases 1 to 705)
  AUTHORS   Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
            Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-APR-1998) Division of Infectious Disease, Affymetrix,
            3380 Central Expressway, Santa Clara, CA 95051, USA
FEATURES             Location/Qualifiers
     source          1. .705
                     /organism="Mycobacterium tuberculosis"
                     /strain="ATCC27294"
                     /db_xref="ATCC:27294"
                     /db_xref="taxon:1773"
     gene            <1. .>705
                     /gene="rpoB"
     CDS             <1. .>705
                     /gene="rpoB"
                     /codon_start=3
                     /transl_table=11
                     /product="RNA polymerase beta-subunit"
                     /protein_id="AAC38533.1"
                     /db_xref="GI:3133465"
                     /translation="QDVEAITPQTLINIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLT
                     HKRRLSALGPGGLSRERAGLEVRDVHPSHYGRMCPIETPEGPNIGLIGSLSVYARVNP
                     FGFIETPYRKVVDGVVSDEIVYLTADEEDRHVVAQANSPIDADGRFVEPRVLVRRKAG
                     EVEYVPSSEVDYMDVSPRQMVSVATAMIPFLEHDDANRALMGANMQRQAVPLVRSEAP
                     LVGTGMELRAAIDAAT"
BASE COUNT      117 a    227 c    250 g    111 t
ORIGIN
```

```
  Query Match           100.0%;  Score 20;  DB 1;  Length 705;
  Best Local Similarity  100.0%;  Pred. No. 1.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    331 TACGGCGTTTCGATGAACCC 312
```

```
RESULT  10
AR149128/c
LOCUS       AR149128                706 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 24 from patent US 6228575.
ACCESSION   AR149128
VERSION     AR149128.1  GI:15113719
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 706)
  AUTHORS   Gingeras,T.R., Mack,D., Chee,M.S., Berno,A.J., Stryer,L.,
            Ghandour,G. and Wang,C.
  TITLE     Chip-based species identification and phenotypic characterization
            of microorganisms
  JOURNAL   Patent: US 6228575-A 24 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .706
                     /organism="unknown"
BASE COUNT      117 a    227 c    250 g    111 t      1 others
ORIGIN
```

```
  Query Match           100.0%;  Score 20;  DB 6;  Length 706;
  Best Local Similarity  100.0%;  Pred. No. 1.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    332 TACGGCGTTTCGATGAACCC 313
```

```
RESULT  11
I50706/c
LOCUS       I50706                  970 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1 from patent US 5643723.
ACCESSION   I50706
VERSION     I50706.1  GI:2472409
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 970)
  AUTHORS   Persing,D.H., Hunt,J.J., Young,K.K.Y., Felmlee,T.A., Roberts,G.D.
            and Whelan,A.Christian.
  TITLE     Detection of a genetic locus encoding resistance to rifampin in
            mycobacterial cultures and in clinical specimens
  JOURNAL   Patent: US 5643723-A 1 01-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .970
                     /organism="unknown"
BASE COUNT      182 a    302 c    330 g    156 t
ORIGIN
```

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  Query Match           100.0%;  Score 20;  DB 6;  Length 970;
  Best Local Similarity  100.0%;  Pred. No. 1.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    671 TACGGCGTTTCGATGAACCC 652
```

```
RESULT  12
AX111339/c
LOCUS       AX111339                3534 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 2072 from Patent WO0123604.
ACCESSION   AX111339
VERSION     AX111339.1  GI:13927631
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 3534)
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 2072 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .3534
                     /organism="Mycobacterium tuberculosis"
                     /strain="Rv"
                     /db_xref="taxon:1773"
BASE COUNT      679 a   1081 c   1188 g    586 t
ORIGIN
```

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  Query Match           100.0%;  Score 20;  DB 6;  Length 3534;
  Best Local Similarity  100.0%;  Pred. No. 1.9;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db   1547 TACGGCGTTTCGATGAACCC 1528


RESULT  13
MTU12205/c
LOCUS       MTU12205                3853 bp    DNA     linear   BCT 02-MAR-2000
DEFINITION  Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
            gene, partial cds.
ACCESSION   U12205
VERSION     U12205.1  GI:515684
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 3853)
  AUTHORS   Imboden,P., Troller,R., Marchesi,F., Telenti,A., Bodmer,T.,
            Cole,S., Schopfer,K. and Burkart,T.
  TITLE     The rpoB gene of Mycobacterium tuberculosis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3853)
  AUTHORS   Imboden,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-1994) Paul Imboden, Institute for Medical
            Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
            3010, Switzerland
FEATURES             Location/Qualifiers
     source          1. .3853
                     /organism="Mycobacterium tuberculosis"
                     /strain="H37Rv"
                     /db_xref="taxon:1773"
     gene            576. .>3853
                     /gene="rpoB"
     CDS             576. .>3853
                     /gene="rpoB"
                     /codon_start=1
                     /transl_table=11
                     /product="RNA-polymerase beta subunit"
                     /protein_id="AAA20242.2"
                     /db_xref="GI:7144499"
                     /translation="MLEGCILADSRQSKTAASPSPSRPQSSSNNSVPGAPNRVSFAKL
                     REPLEVPGLLDVQTDSFEWLIGSPRWRESAAERGDVNPVGGLEEVLYELSPIEDFSGS
                     MSLSFSDPRFDDVKAPVDECKDKDMTYAAPLFVTAEFINNNTGEIKSQTVFMGDFPMM
                     TEKGTFIINGTERVVVSQLVRSPGVYFDETIDKSTDKTLHSVKVIPSRGAWLEFDVDK
                     RDTVGVRIDRKRRQPVTVLLKALGWTSEQIVERFGFSEIMRSTLEKDNTVGTDEALLD
                     IYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARVGRYKVNKKLGLHVGEPITSSTLT
                     EEDVVATIEYLVRLHEGQTTMTVPGGVEVPVETDDIDHFGNRRLRTVGELIQNQIRVG
                     MSRMERVVRERMTTQDVEAITPQTLINIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLT
                     HKRRLSALGPGGLSRERAGLEVRDVHPSHYGRMCPIETPEGPNIGLIGSLSVYARVNP
                     FGFIETPYRKVVDGVVSDGIVYLTADEEDRHVVAQANSPIDADGRFVEPRVLVRRKAG
                     EVEYVPSSEVDYMDVSPRQMVSVATAMIPFLEHDDANRALMGANMQRQAVPLVRSEAP
                     LVGTGMELRAAIDAATSSSQESGVIEEVSADYITVMHDNGTRRTYRMRKFARSNHGTC
                     ANQCPIVDAGDRVEAGQVIADGPCTDDGEMALGKNLLVAIMPWEGHNYEDAIILSNRL
                     VEEDVLTSIHIEEHEIDARDTKLGAEEITRDIPNISDEVLADLDERGIVRIGAEVRDG
                     DILVGKVTPKGETELTPEERLLRAIFGEKAREVRDTSLKVPHGESGKVIGIRVFSRED
                     EDELPAGVNELVRVYVAQKRKISDGDKLAGRHGNKGVIGKILPVEDMPFLADGTPVDI
                     ILNTHGVPRRMNIGQILETHLGWCAHSGWKVDAAKGVPDWAARLPDELLEAQPNAIVS
                     TPVFDGAQEAELQGLLSCTLPNRDGDVLVDADGKAMLFDGRSGEPFPYPVTVGYMYIM
                     KLHHLVDDKIHARSTGPYSMITQQPLGGKAQFGGQRFGEMECWAMQAYGAAYTLQELL
                     TIKS"
BASE COUNT      723 a   1173 c   1293 g    664 t
ORIGIN
```

```
  Query Match           100.0%;  Score 20;  DB 1;  Length 3853;
  Best Local Similarity  100.0%;  Pred. No. 2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db   2122 TACGGCGTTTCGATGAACCC 2103


RESULT  14
MSGRPOB/c
LOCUS       MSGRPOB                 5084 bp    DNA     linear   BCT 13-SEP-1994
DEFINITION  Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB)
            gene, complete cds and RNA polymerase beta'-subunit rpoC gene,
            partial cds.
ACCESSION   L27989
VERSION     L27989.1  GI:468333
KEYWORDS    RNA polymerase beta-subunit; rpoB gene.
SOURCE      Mycobacterium tuberculosis (strain Rv) DNA.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 5084)
  AUTHORS   Miller,L.P., Crawford,J.T. and Shinnick,T.M.
  TITLE     The rpoB gene of Mycobacterium tuberculosis
  JOURNAL   Antimicrob. Agents Chemother. 38 (4), 805-811 (1994)
  MEDLINE   94304130
FEATURES             Location/Qualifiers
     source          1. .5084
                     /organism="Mycobacterium tuberculosis"
                     /strain="Rv"
                     /db_xref="taxon:1773"
     gene            1065. .4598
                     /gene="rpoB"
     CDS             1065. .4598
                     /gene="rpoB"
                     /codon_start=1
                     /transl_table=11
                     /evidence=experimental
                     /product="RNA polymerase beta-subunit"
                     /protein_id="AAA21416.1"
                     /db_xref="GI:468334"
                     /translation="MLEGCILADSRQSKTAASPSPSRPQSSSNNSVPGAPNRVSFAKL
                     REPLEVPGLLDVQTDSFEWLIGSPRWRESAAERGDVNPVGGLEEVLYELSPIEDFSGS
                     MSLSFSDPRFDDVKAPVDECKDKDMTYAAPLFVTAEFINNNTGEIKSQTVFMGDFPMM
                     TEKGTFIINGTERVVVSQLVRSPGVYFDETIDKSTDKTLHSVKVIPSRGAWLEFDVDK
                     RDTVGVRIDRKRRQPVTVLLKALGWTSEQIVERFGFSEIMRSTLEKDNTVGTDEALLD
                     IYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARVGRYKVNKKLGLHVGEPITSSTLT
                     EEDVVATIEYLVRLHEGQTTMTVPGGVEVPVETDDIDHFGNRRLRTVGELIQNQIRVG
                     MSRMERVVRERMTTQDVEAITPQTLINIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLT
                     HKRRLSALGPGGLSRERAGLEVRDVHPSHYGRMCPIETPEGPNIGLIGSLSVYARVNP
                     FGFIETPYRKVVDGVVSDEIVYLTADEEDRHVVAQANSPIDADGRFVEPRVLVRRKAG
                     EVEYVPSSEVDYMDVSPRQMVSVATAMIPFLEHDDANRALMGANMQRQAVPLVRSEAP
                     LVGTGMELRAAIDAATSSSQESGVIEEVSADYITVMHDNGTRRTYRMRKFARSNHGTC
                     ANQCPIVDAGDRVEAGQVIADGPCTDDGEMALGKNLLVAIMPWEGHNYEDAIILSNRL
                     VEEDVLTSIHIEEHEIDARDTKLGAEEITRDIPNISDEVLADLDERGIVRIGAEVRDG
                     DILVGKVTPKGETELTPEERLLRAIFGEKAREVRDTSLKVPHGESGKVIGIRVFSRED
                     EDELPAGVNELVRVYVAQKRKISDGDKLAGRHGNKGVIGKILPVEDMPFLADGTPVDI
                     ILNTHGVPRRMNIGQILETHLGWCAHSGWKVDAAKGVPDWAARLPDELLEAHANAIVS
                     TPVFDGAQEAELQGLLSCTLPNRDGDVLVDADGKAMLFDGRSGEPFPYPVTVGYMYIM
                     KLHHLVDDKIHARSTGPYSMITQQPLGGKAQFGGQRFGEMECWAMQAYGAAYTLQELL
                     TIKSDDTVGRVKVYEAIVKGENIPEPGIPESFKVLLKELQSLCLNVEVLSSDGAAIEL
                     REGEDEDLERAAANLGINLSRNESASFEDLA"
     gene            4641. .5084
                     /gene="rpoC"
     CDS             4641. .>5084
                     /gene="rpoC"
                     /codon_start=1
                     /transl_table=11
                     /product="RNA polymerase beta'-subunit"
                     /protein_id="AAA21417.1"
                     /db_xref="GI:537608"
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                     /translation="MLDVNFFDELRIGLATAEDIRQWSYGEVKKPETINYRTLKPEKD
                     GLFCEKIFGPTRDWECYCGKYKRVRFKGIICERCGVEVTRAKVRRERMGHIELAAPVT
                     HIWYFKGVPSRLGYLLDLAPKDLEKIIYFAAYVITSVDEEMRHNEL"
BASE COUNT      969 a   1534 c   1691 g    890 t
ORIGIN


  Query Match           100.0%;  Score 20;  DB 1;  Length 5084;
  Best Local Similarity  100.0%;  Pred. No. 2.1;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db   2611 TACGGCGTTTCGATGAACCC 2592


RESULT 15
AE006964/c
LOCUS       AE006964               19352 bp    DNA     linear   BCT 27-APR-2001
DEFINITION  Mycobacterium tuberculosis CDC1551,  section 50 of 280 of the
            complete genome.
ACCESSION   AE006964 AE000516
VERSION     AE006964.1  GI:13880217
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis CDC1551.
  ORGANISM  Mycobacterium tuberculosis CDC1551
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 19352)
  AUTHORS   Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O.,
            Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E.,
            Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M.,
            Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H.,
            Gill,J., Mikula,A. and Bishai,W.
  TITLE     Whole genome comparison of Mycobacterium tuberculosis clinical and
            laboratory strains
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 19352)
  AUTHORS   Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O.,
            Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E.,
            Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M.,
            Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H.,
            Gill,J., Mikula,A. and Bishai,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-2001) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .19352
                     /organism="Mycobacterium tuberculosis CDC1551"
                     /strain="CDC1551"
                     /db_xref="taxon:83331"
                     /note="clinical strain"
     gene            163. .3699
                     /gene="MT0695"
     CDS             163. .3699
                     /gene="MT0695"
                     /note="similar to GB:L27989 GB:L05910 GB:U12205 SP:P47766
                     PID:149992; identified by sequence similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="DNA-directed RNA polymerase, beta subunit"
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                     /gene="MT0699"
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gene            10957. .11799
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CDS             10957. .11799
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gene            11859. .13487
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CDS             11859. .13487
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                /transl_table=11
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gene            13498. .14436
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CDS             13498. .14436
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                /protein_id="AAK44927.1"
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gene            14439. .15161
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Qy       1 tacggcgtttcgatgaaccc 20
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Db    1709 TACGGCGTTTCGATGAACCC 1690


Search completed: August  7, 2002, 21:51:46
Job time: 23881 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:15:20 ; Search time 4103.44 Seconds
(without alignments)
65.784 Million cell updates/sec

Title: US-09-786-105-3
Perfect score: 20
Sequence: 1 tacggtcggcgagctgatcc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	18.4	92.0	130	10	BM397871	BM397871 5009-0-38
c	2	18.4	92.0	132	10	BM396091	BM396091 5009-0-17
c	3	18.4	92.0	134	10	BM398255	BM398255 5009-0-42
c	4	17.4	87.0	984	12	CNS01GJZ	AL143232 Anopheles
	5	17	85.0	422	10	BE443802	BE443802 WHE1122_B
	6	17	85.0	544	10	BE445100	BE445100 WHE1132_H
	7	17	85.0	558	10	BE444713	BE444713 WHE1137_H
	8	17	85.0	610	9	BE195103	BE195103 HVSMEh008
	9	17	85.0	658	10	BE442518	BE442518 WHE1101_H
	10	17	85.0	828	10	BG299722	BG299722 HVSMEa002
c	11	16.8	84.0	419	10	BI188703	BI188703 d2e05fs.r
c	12	16.8	84.0	606	10	BI981973	BI981973 fu53f08.y
c	13	16.8	84.0	640	10	BI888442	BI888442 ZF637-2-0
	14	16.4	82.0	292	9	AW502654	AW502654 UI-HF-BR0
	15	16.4	82.0	338	9	AW501791	AW501791 UI-HF-BR0
c	16	16.4	82.0	402	9	BE101908	BE101908 UI-R-BO1-
	17	16.4	82.0	460	9	AW502300	AW502300 UI-HF-BR0
	18	16.4	82.0	470	9	AW502130	AW502130 UI-HF-BR0
	19	16.4	82.0	586	10	BM321268	BM321268 rockefell
	20	16.4	82.0	653	10	BM320964	BM320964 rockefell
	21	16.4	82.0	712	10	BM321334	BM321334 rockefell
	22	16.4	82.0	899	10	BM320891	BM320891 rockefell
	23	16	80.0	708	10	BE585978	BE585978 Est#7pT7_
	24	15.8	79.0	197	6	BE599873	Be599873 PI1_80_G0
	25	15.8	79.0	197	10	BM318366	BM318366 PI1_77_G0
c	26	15.8	79.0	315	10	BE419003	BE419003 WWR020.D1
	27	15.8	79.0	360	10	BG412215	BG412215 OV2_39_C0
c	28	15.8	79.0	411	10	BG263401	BG263401 WHE2341_E
c	29	15.8	79.0	428	9	AI967080	AI967080 496021E08
c	30	15.8	79.0	451	10	C72862	C72862 C72862 Rice
c	31	15.8	79.0	461	10	C28055	C28055 C28055 Rice
c	32	15.8	79.0	493	9	BE215753	BE215753 HV_CEb000
	33	15.8	79.0	507	6	BE599649	Be599649 PI1_78_A0
	34	15.8	79.0	507	10	BM318224	BM318224 PI1_79_A0
	35	15.8	79.0	560	10	BG411877	BG411877 OV2_39_C0
	36	15.8	79.0	565	12	AZ178000	AZ178000 SP_0149_A
c	37	15.8	79.0	597	12	BH402082	BH402082 AG-ND-156
	38	15.8	79.0	605	9	AL508804	AL508804 AL508804
c	39	15.8	79.0	672	9	BB316372	BB316372 BB316372
c	40	15.8	79.0	726	12	AZ359615	AZ359615 1M0102G02
	41	15.8	79.0	740	12	BH016284	BH016284 TDGCK39TH
	42	15.8	79.0	841	10	BI544719	BI544719 603242678
c	43	15.8	79.0	880	10	BI911230	BI911230 603062995
	44	15.8	79.0	946	10	BG475629	BG475629 602520553
c	45	15.8	79.0	1077	12	CNS07739	AL432187 T3 end of

ALIGNMENTS

RESULT 1
BM397871/c
LOCUS BM397871 130 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-38-C10.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM397871
VERSION BM397871.1 GI:18197924
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 130)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel ,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .130
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT 26 a 41 c 44 g 18 t 1 others
ORIGIN

Query Match 92.0%; Score 18.4; DB 10; Length 130;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;

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  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
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Db     94 TACCGTCGGCGAGCTGATCC 75


RESULT   2
BM396091/c
LOCUS       BM396091                132 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-17-B01.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM396091
VERSION     BM396091.1  GI:18196144
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila.
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1  (bases 1 to 132)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
            ,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .132
                     /organism="Tetrahymena thermophila"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT       27 a     42 c     44 g     19 t
ORIGIN


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  Best Local Similarity   95.0%;  Pred. No. 1.7e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
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Db     96 TACCGTCGGCGAGCTGATCC 77


RESULT   3
BM398255/c
LOCUS       BM398255                134 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-42-H08.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM398255
VERSION     BM398255.1  GI:18198308
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila.
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1  (bases 1 to 134)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
            ,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
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                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT       26 a     44 c     46 g     18 t
ORIGIN


  Query Match             92.0%;  Score 18.4;  DB 10;  Length 134;
  Best Local Similarity   95.0%;  Pred. No. 1.7e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||| ||||||||||||||||
Db     98 TACCGTCGGCGAGCTGATCC 79


RESULT   4
CNS01GJZ/c
LOCUS       CNS01GJZ                984 bp    DNA     linear   GSS 01-JUN-2001
DEFINITION  Anopheles gambiae GSS T7 end of clone 06016 of NotreDame1 library
            from strain PEST of Anopheles gambiae (African malaria mosquito),
            genomic survey sequence.
ACCESSION   AL143232
VERSION     AL143232.1  GI:7001389
KEYWORDS    GSS.
SOURCE      African malaria mosquito.
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
            Culicoidea; Anopheles.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
REFERENCE   2  (bases 1 to 984)
  AUTHORS   Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
            Roux, Paris 75015, France
COMMENT     This clone is from an A. gambiae BAC library provided by F.H.
            Collins and sequenced by Genoscope in collaboration with the
            Laboratory of Biochem. and Biol. Molec. of Insects, Institut
            Pasteur.
FEATURES             Location/Qualifiers
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                     /strain="PEST"
                     /db_xref="taxon:7165"
                     /clone="06016"
                     /clone_lib="NotreDame1"
                     /note="end : T7"
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ORIGIN


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  Best Local Similarity   94.7%;  Pred. No. 7.4e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy      1 tacggtcggcgagctgatc 19
          ||||||||||||||| |||
Db    103 TACGGTCGGCGAGCTAATC 85


RESULT   5
BE443802
LOCUS       BE443802                422 bp    mRNA    linear   EST 25-JUL-2000
DEFINITION  WHE1122_B06_C12ZS Wheat etiolated seedling root normalized cDNA
            library Triticum aestivum cDNA clone WHE1122_B06_C12, mRNA
            sequence.
ACCESSION   BE443802
VERSION     BE443802.1  GI:9443341
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 422)
  AUTHORS   Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
            ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
            Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Normalized root cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES             Location/Qualifiers
     source          1. .422
                     /organism="Triticum aestivum"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="WHE1122_B06_C12"
                     /clone_lib="Wheat etiolated seedling root normalized cDNA
                     library"
                     /tissue_type="Root"
                     /dev_stage="Five day old etiolated seedling"
                     /lab_host="E. coli DH10B"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid
                     pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
                     surface-sterilized, germinated and grown aseptically in
                     the  dark at room temperature on filter paper with water,
                     nystatin and  cefotaxime in covered crystallization
                     dishes. Roots were harvested.  The tissue, total RNA, and
                     poly(A) RNA were prepared, a cDNA library  was made in the
                     TJ Close lab (Choi, Close, Fenton) at the University  of
                     California, Riverside.  The cDNA clones were in vivo
                     excised to  give pBluescript phagemids before
                     normalization was carried out.   The mass excision of
                     phagemid library and normalization were done in HT  Nguyen
                     lab by D. Zhang at Texas Tech Univeristy.  Normalization
                     protocol used was that of Soares.  Plasmid DNA
                     preparations and DNA  sequencing were performed in the OD
                     Anderson lab (all other authors)."
BASE COUNT       84 a    130 c    124 g     84 t
ORIGIN


  Query Match            85.0%;  Score 17;  DB 10;  Length 422;
  Best Local Similarity  100.0%;  Pred. No. 9.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggtcggcgagctgatcc 20
          |||||||||||||||||
Db     86 GGTCGGCGAGCTGATCC 102


RESULT   6
BE445100
LOCUS       BE445100                544 bp    mRNA    linear   EST 25-JUL-2000
DEFINITION  WHE1132_H08_P16ZS Wheat etiolated seedling root normalized cDNA
            library Triticum aestivum cDNA clone WHE1132_H08_P16, mRNA
            sequence.
ACCESSION   BE445100
VERSION     BE445100.1  GI:9444655
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 544)
  AUTHORS   Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
            ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
            Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Normalized root cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES             Location/Qualifiers
     source          1. .544
                     /organism="Triticum aestivum"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="WHE1132_H08_P16"
                     /clone_lib="Wheat etiolated seedling root normalized cDNA
                     library"
                     /tissue_type="Root"
                     /dev_stage="Five day old etiolated seedling"
                     /lab_host="E. coli DH10B"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid
                     pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
                     surface-sterilized, germinated and grown aseptically in
                     the  dark at room temperature on filter paper with water,
                     nystatin and  cefotaxime in covered crystallization
                     dishes. Roots were harvested.  The tissue, total RNA, and
                     poly(A) RNA were prepared, a cDNA library  was made in the
                     TJ Close lab (Choi, Close, Fenton) at the University  of
                     California, Riverside.  The cDNA clones were in vivo
                     excised to  give pBluescript phagemids before
                     normalization was carried out.   The mass excision of
                     phagemid library and normalization were done in HT  Nguyen
                     lab by D. Zhang at Texas Tech Univeristy.  Normalization
                     protocol used was that of Soares.  Plasmid DNA
                     preparations and DNA  sequencing were performed in the OD
                     Anderson lab (all other authors)."
BASE COUNT      121 a    173 c    132 g    118 t
ORIGIN


  Query Match            85.0%;  Score 17;  DB 10;  Length 544;
  Best Local Similarity  100.0%;  Pred. No. 9.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggtcggcgagctgatcc 20
          |||||||||||||||||
Db    512 GGTCGGCGAGCTGATCC 528
```

```
RESULT   7
BE444713
LOCUS       BE444713                 558 bp    mRNA    linear   EST 25-JUL-2000
DEFINITION  WHE1137_H03_O05ZS Wheat etiolated seedling root normalized cDNA
            library Triticum aestivum cDNA clone WHE1137_H03_O05, mRNA
            sequence.
ACCESSION   BE444713
VERSION     BE444713.1  GI:9444264
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 558)
  AUTHORS   Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
            ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
            Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Normalized root cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES             Location/Qualifiers
     source          1. .558
                     /organism="Triticum aestivum"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="WHE1137_H03_O05"
                     /clone_lib="Wheat etiolated seedling root normalized cDNA
                     library"
                     /tissue_type="Root"
                     /dev_stage="Five day old etiolated seedling"
                     /lab_host="E. coli DH10B"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid
                     pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
                     surface-sterilized, germinated and grown aseptically in
                     the  dark at room temperature on filter paper with water,
                     nystatin and  cefotaxime in covered crystallization
                     dishes. Roots were harvested.  The tissue, total RNA, and
                     poly(A) RNA were prepared, a cDNA library  was made in the
                     TJ Close lab (Choi, Close, Fenton) at the University  of
                     California, Riverside.  The cDNA clones were in vivo
                     excised to  give pBluescript phagemids before
                     normalization was carried out.  The mass excision of
                     phagemid library and normalization were done in HT  Nguyen
                     lab by D. Zhang at Texas Tech Univeristy.  Normalization
                     protocol used was that of Soares.  Plasmid DNA
                     preparations and DNA  sequencing were performed in the OD
                     Anderson lab (all other authors)."
BASE COUNT      122 a    180 c    134 g    122 t
ORIGIN

  Query Match             85.0%;  Score 17;  DB 10;  Length 558;
  Best Local Similarity   100.0%;  Pred. No. 9.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggtcggcgagctgatcc 20
          |||||||||||||||||
Db    514 GGTCGGCGAGCTGATCC 530


RESULT   8
```

```
BE195103
LOCUS       BE195103                 610 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEh0088E21f Hordeum vulgare 5-45 DAP spike EST library
            HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0088E21f,
            mRNA sequence.
ACCESSION   BE195103
VERSION     BE195103.3  GI:16321083
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 610)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
            ,R.D., Close,S.J., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex 5-45 DAP spike cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     On Jun 26, 2000 this sequence version replaced gi:13187931.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 238
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 563.
FEATURES             Location/Qualifiers
     source          1. .610
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEh0088E21f"
                     /clone_lib="Hordeum vulgare 5-45 DAP spike EST library
                     HVcDNA0009 (5 to 45 DAP)"
                     /tissue_type="5-45 DAP Spike"
                     /lab_host="SOLR"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     Plants were grown in the greenhouse at the University of
                     California, Riverside (Fenton, SJ Close, TJ Close). Whole
                     spikes with awns trimmed were collected at 5, 10, 15, 20,
                     30 and 45 DAP (Fenton). Total RNA was prepared from each
                     pool, equal quantities of all six RNA pools were combined,
                     poly(A) RNA was purified from the mixture, one primary
                     unamplified cDNA library was made, and 1 million pfu were
                     in vivo excised to give pBluescript SK(-) cDNA phagemids
                     (Choi)in the TJ Close lab at the University of California,
                     Riverside. Phagemids were plated and picked at the Clemson
                     University Genomics Institute (CUGI) (Begum, Palmer,
                     Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
                     sequencing and sequence analysis were performed at CUGI
                     (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
                     The sequence has been trimmed to remove vector sequence
                     and contains a minimum of 100 bases of phred value 20 or
                     above. For more details on library preparation and
                     sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      127 a    203 c    158 g    120 t      2 others
ORIGIN

  Query Match             85.0%;  Score 17;  DB 9;  Length 610;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy      4 ggtcggcgagctgatcc 20
          ||||||||||||||||||
Db    499 GGTCGGCGAGCTGATCC 515


RESULT  9
BE442518
LOCUS       BE442518                 658 bp    mRNA    linear   EST 25-JUL-2000
DEFINITION  WHE1101_H10_O19ZS Wheat etiolated seedling root normalized cDNA
            library Triticum aestivum cDNA clone WHE1101_H10_O19, mRNA
            sequence.
ACCESSION   BE442518
VERSION     BE442518.1  GI:9442034
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 658)
  AUTHORS   Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
            ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
            Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Normalized root cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES             Location/Qualifiers
     source          1. .658
                     /organism="Triticum aestivum"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="WHE1101_H10_O19"
                     /clone_lib="Wheat etiolated seedling root normalized cDNA
                     library"
                     /tissue_type="Root"
                     /dev_stage="Five day old etiolated seedling"
                     /lab_host="E. coli DH10B"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid
                     pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
                     surface-sterilized, germinated and grown aseptically in
                     the  dark at room temperature on filter paper with water,
                     nystatin and  cefotaxime in covered crystallization
                     dishes. Roots were harvested.  The tissue, total RNA, and
                     poly(A) RNA were prepared, a cDNA library  was made in the
                     TJ Close lab (Choi, Close, Fenton) at the University  of
                     California, Riverside.  The cDNA clones were in vivo
                     excised to  give pBluescript phagemids before
                     normalization was carried out.  The mass excision of
                     phagemid library and normalization were done in HT  Nguyen
                     lab by D. Zhang at Texas Tech Univeristy.  Normalization
                     protocol used was that of Soares.  Plasmid DNA
                     preparations and DNA  sequencing were performed in the OD
                     Anderson lab (all other authors)."
BASE COUNT      144 a    209 c    165 g    140 t
ORIGIN


  Query Match             85.0%;  Score 17;  DB 10;  Length 658;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggtcggcgagctgatcc 20
          ||||||||||||||||||
Db    512 GGTCGGCGAGCTGATCC 528


RESULT  10
BG299722
LOCUS       BG299722                 828 bp    mRNA    linear   EST 17-OCT-2001
DEFINITION  HVSMEa0021I20f Hordeum vulgare seedling shoot EST library
            HVcDNA0001 (Cold stress) Hordeum vulgare cDNA clone HVSMEa0021I20f,
            mRNA sequence.
ACCESSION   BG299722
VERSION     BG299722.1  GI:13087434
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 828)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R., Choi,D.W.
            , Fenton,R.D. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex cold-stressed seedling shoot cDNA
            library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 574
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 643.
FEATURES             Location/Qualifiers
     source          1. .828
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEa0021I20f"
                     /clone_lib="Hordeum vulgare seedling shoot EST library
                     HVcDNA0001 (Cold stress)"
                     /tissue_type="Seedling shoot"
                     /lab_host="TJC121"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     Seeds were surface sterilized then germinated under axenic
                     conditions in the dark at room temperature on filter paper
                     with water, nystatin and cefotaxime in covered
                     crystallization dishes. Five-day old seedlings were
                     incubated at 5oC for 2 days. Shoots were then harvested,
                     total RNA was prepared, poly(A) RNA was purified, one
                     primary unamplified cDNA library was made, and 600000 pfu
                     were in vivo excised to give pBluescript SK(-) cDNA
                     phagemids. These steps were performed in the TJ Close
                     laboratory at the University of California, Riverside
                     (Choi, Close, Fenton). Phagemids were plated and picked at
                     the Clemson University Genomics Institute (CUGI) (Begum,
                     Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations
                     , DNA sequencing and sequence analysis were performed at
                     CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main
                     ). The sequence has been trimmed to remove vector sequence
                     and contains a minimum of 100 bases of phred value 20 or
                     above. For more details on library preparation and
                     sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      172 a    271 c    220 g    165 t
```

```
ORIGIN


  Query Match             85.0%;  Score 17;  DB 10;  Length 828;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggtcggcgagctgatcc 20
          |||||||||||||||||
Db    500 GGTCGGCGAGCTGATCC 516


RESULT  11
BI188703/c
LOCUS       BI188703                 419 bp    mRNA    linear   EST 10-JUL-2001
DEFINITION  d2e05fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
            library Fusarium sporotrichioides cDNA clone d2e05fs 5', mRNA
            sequence.
ACCESSION   BI188703
VERSION     BI188703.1  GI:14662382
KEYWORDS    EST.
SOURCE      Fusarium sporotrichioides.
  ORGANISM  Fusarium sporotrichioides
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; mitosporic Hypocreales; Fusarium.
REFERENCE   1  (bases 1 to 419)
  AUTHORS   Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
            ,M. and Roe,B.
  TITLE     Analysis of a Fusarium sporotrichioides EST database
  JOURNAL   Unpublished (2001)
COMMENT     Other_ESTs: d2e05fs.f1
            Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
            Department of Chemistry and Biochemistry
            Advanced Center for Genome Technology, University of Oklahoma
            620 Parrington Oval, Norman, OK 73019, USA
            Tel: 405 325 4912
            Fax: 405 325 7762
            Email: broe@ou.edu
            Contact Dr. Marian Beremand regarding clone availability Included
            is the best homolog from a blastx search of Genbank nr 04-09-01
            73 2.2 gi|7799258|emb|CAB90 (AL355752) putative integral
            membraneprote
            Seq primer: T3
            High quality sequence stop: 107.
FEATURES             Location/Qualifiers
     source          1. .419
                     /organism="Fusarium sporotrichioides"
                     /strain="Tri 10"
                     /db_xref="taxon:5514"
                     /clone="d2e05fs"
                     /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
                     cDNA library"
                     /note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2:
                     XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
                     ; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT      117 a    106 c    117 g     79 t
ORIGIN


  Query Match             84.0%;  Score 16.8;  DB 10;  Length 419;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||| ||||||| ||||
Db    114 TACGGTCAGCGAGCTCATCC 95


RESULT  12
BI981973/c
LOCUS       BI981973                 606 bp    mRNA    linear   EST 24-OCT-2001
DEFINITION  fu53f08.y1 zebrafish adult brain Danio rerio cDNA clone 5333151 5'
            similar to TR:Q9Y4D4 Q9Y4D4 KIAA0648 PROTEIN ;, mRNA sequence.
ACCESSION   BI981973
VERSION     BI981973.1  GI:16371108
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 606)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
            ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
            ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
            Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
            Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
            and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Other_ESTs: fu53f08.x1
            Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
            Matthew Clark. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
            www.rzpd.de)
            High quality sequence stop: 446.
FEATURES             Location/Qualifiers
     source          1. .606
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone="5333151"
                     /clone_lib="zebrafish adult brain"
                     /sex="mixed male and female"
                     /tissue_type="brain"
                     /dev_stage="adult"
                     /lab_host="E. coli DH10B"
                     /note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
                     Original library was constructed in lambdaZIPLOX.  Mass
                     excision of the cDNA library was performed to yield
                     pZIPLOX plasmids. Insert check was done in original
                     library."
BASE COUNT      209 a    133 c    139 g    125 t
ORIGIN


  Query Match             84.0%;  Score 16.8;  DB 10;  Length 606;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          |||||||||||||||| | |
Db    452 TACGGTCGGCGAGCTGTTAC 433


RESULT  13
BI888442/c
LOCUS       BI888442                 640 bp    mRNA    linear   EST 12-OCT-2001
DEFINITION  ZF637-2-000197 Zebrafish shield stage whole embryo cDNA library
            MPMGp637 Danio rerio cDNA clone MPMGp637_18E17;MPMGp637E1718 5',
            mRNA sequence.
ACCESSION   BI888442
VERSION     BI888442.1  GI:16095713
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 640)
  AUTHORS   Clark,M., Aanstad,P., Hennig,S., Johnson,S.L. and Lehrach,H.
  TITLE     EST sequencing of a zebrafish shield stage cDNA library normalised
            by oligonucleotide fingerprinting
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Hennig S
            laboraty 123, dept.Lehrach
            Max-Planck-Institut fuer Molekulare Genetik
            Ihnestr.63-73, D-14195 Berlin, Germany
            Tel: +49 30 8413 1612
            Fax: +49 30 8413 1380
            Email: hennig@molgen.mpg.de
            5' EST sequencing of clones from a zebrafish shield stage library,
            normalised from 55,000 starting clones by oligonucleotide
            fingerprinting
            High quality sequence stop: 640.
FEATURES             Location/Qualifiers
     source          1. .640
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone="MPMGp637_18E17;MPMGp637E1718"
                     /clone_lib="Zebrafish shield stage whole embryo cDNA
                     library MPMGp637"
                     /tissue_type="whole embryo"
                     /dev_stage="shield stage, 6 hrs post-fertilisation"
                     /lab_host="E.coli, XL1 blue MRF"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI;
                     oligo-dT-NotI primed, SalI adaptors, directionally cloned,
                     library normalised by oligonucleotide fingerprinting"
BASE COUNT      209 a    152 c    139 g    139 t      1 others
ORIGIN


  Query Match             84.0%;  Score 16.8;  DB 10;  Length 640;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          |||||||||||||||| | |
Db    541 TACGGTCGGCGAGCTGTTAC 522


RESULT  14
AW502654
LOCUS       AW502654                292 bp    mRNA    linear   EST 01-MAR-2000
DEFINITION  UI-HF-BR0p-ajx-b-11-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone
            IMAGE:3075813 5', mRNA sequence.
ACCESSION   AW502654
VERSION     AW502654.1  GI:7117309
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 292)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .292
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3075813"
                     /clone_lib="NIH_MGC_52"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (7.4-9.5kb).  Directionally cloned. Cells provided by
                     Louis M. Staudt, Ph.D.  Library preparation by Maria de
                     Fatima Bonaldo, Ph.D. and  M. Bento Soares, Ph.D. "
BASE COUNT       51 a     84 c    105 g     52 t
ORIGIN


  Query Match             82.0%;  Score 16.4;  DB 9;  Length 292;
  Best Local Similarity   94.4%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 acggtcggcgagctgatc 19
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Db     46 ACGGTCGGCGTGCTGATC 63


RESULT  15
AW501791
LOCUS       AW501791                338 bp    mRNA    linear   EST 01-MAR-2000
DEFINITION  UI-HF-BR0p-ajm-g-11-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone
            IMAGE:3075260 5', mRNA sequence.
ACCESSION   AW501791
VERSION     AW501791.1  GI:7115654
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 338)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .338
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3075260"
                     /clone_lib="NIH_MGC_52"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (7.4-9.5kb).  Directionally cloned. Cells provided by
                     Louis M. Staudt, Ph.D.  Library preparation by Maria de
                     Fatima Bonaldo, Ph.D. and  M. Bento Soares, Ph.D. "
BASE COUNT       56 a     98 c    124 g     60 t
ORIGIN


  Query Match             82.0%;  Score 16.4;  DB 9;  Length 338;
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Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2 acggtcggcgagctgatc 19
           |||||||||| |||||||
Db      46 ACGGTCGGCGTGCTGATC 63
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Search completed: August 7, 2002, 21:15:21
Job time: 22891 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:54:16 ; Search time 146.61 Seconds
(without alignments)
33.508 Million cell updates/sec

Title: US-09-786-105-2
Perfect score: 20
Sequence: 1 tacggcgtttcgatgaaccc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	20	100.0	432	2	US-08-313-185-59	Sequence 59, Appl
c	2	20	100.0	432	3	US-09-082-614A-59	Sequence 59, Appl
c	3	20	100.0	620	2	US-08-757-653-135	Sequence 135, App
c	4	20	100.0	620	2	US-08-757-653-136	Sequence 136, App
c	5	20	100.0	620	2	US-08-757-653-137	Sequence 137, App
	6	20	100.0	620	2	US-08-757-653-138	Sequence 138, App
	7	20	100.0	620	2	US-08-757-653-139	Sequence 139, App
	8	20	100.0	620	2	US-08-757-653-140	Sequence 140, App
c	9	20	100.0	706	4	US-08-797-812-24	Sequence 24, Appl
c	10	20	100.0	970	1	US-08-250-030-1	Sequence 1, Appli
c	11	20	100.0	970	5	PCT-US95-06790-1	Sequence 1, Appli
	12	19	95.0	19	4	US-08-750-088A-71	Sequence 71, Appl
c	13	18.4	92.0	3447	2	US-08-313-185-57	Sequence 57, Appl
c	14	18.4	92.0	3447	3	US-09-082-614A-57	Sequence 57, Appl
c	15	15.8	79.0	1472	1	US-08-622-354-2	Sequence 2, Appli
c	16	15.8	79.0	2310	1	US-08-622-354-1	Sequence 1, Appli
	17	15.2	76.0	4403765	4	US-09-103-840A-2	Sequence 2, Appli
	18	15	75.0	27	1	US-08-250-030-9	Sequence 9, Appli
	19	15	75.0	27	5	PCT-US95-06790-9	Sequence 9, Appli
	20	14.2	71.0	1081	4	US-09-372-422A-33	Sequence 33, Appl
	21	14.2	71.0	1153	4	US-09-372-448A-5	Sequence 5, Appli
	22	14.2	71.0	2262	2	US-08-674-887A-5	Sequence 5, Appli
	23	14.2	71.0	2262	3	US-08-951-844-5	Sequence 5, Appli
c	24	13.8	69.0	117	1	US-08-299-498A-59	Sequence 59, Appl
c	25	13.8	69.0	117	5	PCT-US95-10813-59	Sequence 59, Appl
	26	13.8	69.0	776	4	US-09-372-422A-43	Sequence 43, Appl
	27	13.8	69.0	1100	4	US-09-372-422A-47	Sequence 47, Appl
c	28	13.8	69.0	1176	3	US-08-911-853-34	Sequence 34, Appl
c	29	13.8	69.0	1176	4	US-09-479-409-34	Sequence 34, Appl
c	30	13.8	69.0	1176	4	US-09-479-453-34	Sequence 34, Appl
	31	13.8	69.0	1375	4	US-09-372-422A-37	Sequence 37, Appl
	32	13.8	69.0	1485	4	US-09-372-422A-39	Sequence 39, Appl
	33	13.8	69.0	2394	3	US-09-027-064-1	Sequence 1, Appli
	34	13.8	69.0	2394	4	US-09-271-815-1	Sequence 1, Appli
c	35	13.8	69.0	17612	3	US-08-911-853-29	Sequence 29, Appl
c	36	13.8	69.0	17612	4	US-09-479-409-29	Sequence 29, Appl
c	37	13.8	69.0	17612	4	US-09-479-453-29	Sequence 29, Appl
c	38	13.8	69.0	4403765	4	US-09-103-840A-2	Sequence 2, Appli
	39	13.6	68.0	585	4	US-09-404-671-3	Sequence 3, Appli
	40	13.6	68.0	686	4	US-09-372-422A-45	Sequence 45, Appl
c	41	13.6	68.0	699	4	US-08-998-416-705	Sequence 705, App
c	42	13.6	68.0	999	4	US-09-177-234-7	Sequence 7, Appli
	43	13.6	68.0	1087	4	US-09-372-422A-29	Sequence 29, Appl
	44	13.6	68.0	1209	1	US-08-314-309A-5	Sequence 5, Appli
	45	13.6	68.0	1513	1	US-08-314-309A-2	Sequence 2, Appli

ALIGNMENTS

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RESULT   1
US-08-313-185-59/c
; Sequence 59, Application US/08313185
; Patent No. 5851763
;  GENERAL INFORMATION:
;    APPLICANT:  Heym, Beate
;    APPLICANT:  Cole, Stewart
;    APPLICANT:  Young, Douglas
;    APPLICANT:  Zhang, Ying
;    APPLICANT:  Honore, Nadine
;    APPLICANT:  Telenti, Amalio
;    APPLICANT:  Bodmer, Thomas
;    TITLE OF INVENTION:  Rapid Detection of Antibiotic Resistance
;    TITLE OF INVENTION:  in Mycobacterium Tuberculosis
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/313,185
;      FILING DATE:  12-OCT-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  02356.0068-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-313-185-59


  Query Match             100.0%;  Score 20;  DB 2;  Length 432;
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  Best Local Similarity   100.0%;  Pred. No. 0.033;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
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Db     428 TACGGCGTTTCGATGAACCC 409


RESULT   2
US-09-082-614A-59/c
; Sequence 59, Application US/09082614A
; Patent No. 6124098
;  GENERAL INFORMATION:
;    APPLICANT:  Heym, Beate
;    APPLICANT:  Cole, Stewart
;    APPLICANT:  Young, Douglas
;    APPLICANT:  Zhang, Ying
;    APPLICANT:  Honore, Nadine
;    APPLICANT:  Telenti, Amalio
;    APPLICANT:  Bodmer, Thomas
;    TITLE OF INVENTION:  Rapid Detection of Antibiotic Resistance
;    TITLE OF INVENTION:  in Mycobacterium Tuberculosis
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/082,614A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/313,185
;      FILING DATE:  12-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  02356.0068-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-082-614A-59


  Query Match             100.0%;  Score 20;  DB 3;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 0.033;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
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Db     428 TACGGCGTTTCGATGAACCC 409


RESULT   3
US-08-757-653-135/c
; Sequence 135, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  135:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-135


  Query Match             100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity   100.0%;  Pred. No. 0.034;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaaccc 20
           ||||||||||||||||||||
Db     296 TACGGCGTTTCGATGAACCC 277


RESULT   4
US-08-757-653-136/c
; Sequence 136, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
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;       APPLICATION NUMBER:  US/08/757,653
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Ingolia, Diane E.
;       REGISTRATION NUMBER:  40,027
;       REFERENCE/DOCKET NUMBER:  FORS-02565
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 705-8410
;       TELEFAX:  (415) 397-8338
;   INFORMATION FOR SEQ ID NO:  136:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  620 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-757-653-136


  Query Match           100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity  100.0%;  Pred. No. 0.034;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    296 TACGGCGTTTCGATGAACCC 277


RESULT   5
US-08-757-653-137/c
; Sequence 137, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  137:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-137


  Query Match           100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity  100.0%;  Pred. No. 0.034;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    296 TACGGCGTTTCGATGAACCC 277


RESULT   6
US-08-757-653-138
; Sequence 138, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  138:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-138


  Query Match           100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity  100.0%;  Pred. No. 0.034;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    325 TACGGCGTTTCGATGAACCC 344


RESULT   7
US-08-757-653-139
; Sequence 139, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  139:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-139


  Query Match             100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity   100.0%;  Pred. No. 0.034;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    325 TACGGCGTTTCGATGAACCC 344


RESULT   8
US-08-757-653-140
; Sequence 140, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  140:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-140


  Query Match             100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity   100.0%;  Pred. No. 0.034;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    325 TACGGCGTTTCGATGAACCC 344


RESULT   9
US-08-797-812-24/c
; Sequence 24, Application US/08797812
; Patent No. 6228575
;  GENERAL INFORMATION:
;    APPLICANT:  Gingeras, Thomas A.
;    APPLICANT:  Mack, David
;    APPLICANT:  Chee, Mark S.
;    APPLICANT:  Berno, Anthony J.
;    APPLICANT:  Stryer, Lubert
;    APPLICANT:  Ghandour, Ghassan
;    APPLICANT:  Wang, Ching
;    TITLE OF INVENTION:  Chip-Based Species Identification and
;    TITLE OF INVENTION:  Phenotypic Characterization of Microorganisms
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/797,812
;      FILING DATE:  07-FEB-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/017,765
;      FILING DATE:  15-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/629,031
;      FILING DATE:  08-APR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/012,631
;      FILING DATE:  01-MAR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,339
;      FILING DATE:  08-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitts, Renee A.
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  16528X-018550
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  24:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  706 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-797-812-24


  Query Match            100.0%;  Score 20;  DB 4;  Length 706;
  Best Local Similarity   100.0%;  Pred. No. 0.035;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    332 TACGGCGTTTCGATGAACCC 313


RESULT  10
US-08-250-030-1/c
; Sequence 1, Application US/08250030
; Patent No. 5643723
;  GENERAL INFORMATION:
;    APPLICANT:  Persing, David H.
;    TITLE OF INVENTION:  Detection of a Genetic Locus Encoding
;    TITLE OF INVENTION:  Resistance to Rifampin in Mycobacterial Cultures and in
;    TITLE OF INVENTION:  Clinical Specimens
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schwegman, Lundberg & Woessner
;      STREET:  3500 IDS Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/250,030
;      FILING DATE:  26-MAY-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueting, Ann M.
;      REGISTRATION NUMBER:  33,977
;      REFERENCE/DOCKET NUMBER:  150.105US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-339-0331
;      TELEFAX:  612-339-3061
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  970 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-250-030-1


  Query Match            100.0%;  Score 20;  DB 1;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 0.036;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    671 TACGGCGTTTCGATGAACCC 652


RESULT  11
PCT-US95-06790-1/c
; Sequence 1, Application PC/TUS9506790
;  GENERAL INFORMATION:
;    APPLICANT:  Mayo Foundation for Medical Education and Research
;    APPLICANT:  and Hoffmann-La Roche Inc.
;    TITLE OF INVENTION:  Detection of a Genetic Locus Encoding
;    TITLE OF INVENTION:  Resistance to Rifampin
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schwegman, Lundberg & Woessner
;      STREET:  3500 IDS Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/06790
;      FILING DATE:  26-MAY-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Raasch, Kevin W.
;      REGISTRATION NUMBER:  35,651
;      REFERENCE/DOCKET NUMBER:  150.105WO1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-339-0331
;      TELEFAX:  612-339-3061
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  970 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
PCT-US95-06790-1


  Query Match            100.0%;  Score 20;  DB 5;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 0.036;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    671 TACGGCGTTTCGATGAACCC 652


RESULT  12
US-08-750-088A-71
; Sequence 71, Application US/08750088A
; Patent No. 6329138
;  GENERAL INFORMATION:
;    APPLICANT:  DE BEENHOUWER, HANS
;    APPLICANT:  PORTAELS, FRAN OISE
;    APPLICANT:  MACHTELINCKX, LIEVE
;    APPLICANT:  JANNES, GEERT
;    APPLICANT:  ROSSAU, RUDI
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF THE ANTIBIOTIC
;    TITLE OF INVENTION:  RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  US
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/750,088A
;      FILING DATE:  21-FEB-1997
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GOLDSTEIN, JORGE A.
;      REGISTRATION NUMBER:  29,021
;      REFERENCE/DOCKET NUMBER:  1657.0010000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-750-088A-71


  Query Match             95.0%;  Score 19;  DB 4;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0.08;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaacc 19
          ||||||||||||||||||||
Db      1 TACGGCGTTTCGATGAACC 19


RESULT  13
US-08-313-185-57/c
; Sequence 57, Application US/08313185
; Patent No. 5851763
;  GENERAL INFORMATION:
;    APPLICANT:  Heym, Beate
;    APPLICANT:  Cole, Stewart
;    APPLICANT:  Young, Douglas
;    APPLICANT:  Zhang, Ying
;    APPLICANT:  Honore, Nadine
;    APPLICANT:  Telenti, Amalio
;    APPLICANT:  Bodmer, Thomas
;    TITLE OF INVENTION:  Rapid Detection of Antibiotic Resistance
;    TITLE OF INVENTION:  in Mycobacterium Tuberculosis
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/313,185
;      FILING DATE:  12-OCT-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  02356.0068-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3447 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-313-185-57


  Query Match             92.0%;  Score 18.4;  DB 2;  Length 3447;
  Best Local Similarity   95.0%;  Pred. No. 0.32;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||| ||||||||||||||
Db   1454 TACGGTGTTTCGATGAACCC 1435


RESULT  14
US-09-082-614A-57/c
; Sequence 57, Application US/09082614A
; Patent No. 6124098
;  GENERAL INFORMATION:
;    APPLICANT:  Heym, Beate
;    APPLICANT:  Cole, Stewart
;    APPLICANT:  Young, Douglas
;    APPLICANT:  Zhang, Ying
;    APPLICANT:  Honore, Nadine
;    APPLICANT:  Telenti, Amalio
;    APPLICANT:  Bodmer, Thomas
;    TITLE OF INVENTION:  Rapid Detection of Antibiotic Resistance
;    TITLE OF INVENTION:  in Mycobacterium Tuberculosis
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/082,614A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/313,185
;      FILING DATE:  12-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  02356.0068-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3447 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-082-614A-57


  Query Match             92.0%;  Score 18.4;  DB 3;  Length 3447;
  Best Local Similarity   95.0%;  Pred. No. 0.32;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||| ||||||||||||||
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Db   1454 TACGGTGTTTCGATGAACCC 1435


RESULT 15
US-08-622-354-2/c
; Sequence 2, Application US/08622354
; Patent No. 5827518
;  GENERAL INFORMATION:
;    APPLICANT:  WEBB, Bruce A.
;    APPLICANT:  CUI, Liwang
;    TITLE OF INVENTION:  VIRAL AND INSECT GENES THAT INHIBIT THE
;    TITLE OF INVENTION:  IMMUNE SYSTEM AND METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LOWE, PRICE, LEBLANC & BECKER
;      STREET:  99 Canal Center Plaza, Suite 300
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/622,354
;      FILING DATE:  27-MAR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Price, Robert L.
;      REGISTRATION NUMBER:  22,685
;      REFERENCE/DOCKET NUMBER:  434-061
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 684-1111
;      TELEFAX:  (703) 684-1124
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1472 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  190..1155
US-08-622-354-2


  Query Match             79.0%;  Score 15.8;  DB 1;  Length 1472;
  Best Local Similarity   89.5%;  Pred. No. 8;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 tacggcgtttcgatgaacc 19
           ||||| |||| ||||||||
Db    1105 TACGGGGTTTAGATGAACC 1087


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Job time: 24016 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:51:38 ; Search time 2167.9 Seconds
(without alignments)
193.058 Million cell updates/sec

Title: US-09-786-105-3
Perfect score: 20
Sequence: 1 tacggtcggcgagctgatcc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
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19: em_mu:*
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21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	306	1	AF057450	AF057450 Mycobacte
2	20	100.0	306	1	AF057451	AF057451 Mycobacte
3	20	100.0	306	1	AF057452	AF057452 Mycobacte
4	20	100.0	306	1	AF057453	AF057453 Mycobacte
5	20	100.0	306	1	AF057454	AF057454 Mycobacte
6	20	100.0	306	6	AR157003	AR157003 Sequence
7	20	100.0	306	6	AR157007	AR157007 Sequence
8	20	100.0	306	6	AR157008	AR157008 Sequence
9	20	100.0	306	6	AR157042	AR157042 Sequence
10	20	100.0	306	6	AR157051	AR157051 Sequence
11	20	100.0	432	1	MSGRIFRNAP	L05910 Mycobacteri
12	20	100.0	432	6	AR067448	AR067448 Sequence
13	20	100.0	970	6	I50706	I50706 Sequence 1
14	20	100.0	3534	6	AX111339	AX111339 Sequence
15	20	100.0	3853	1	MTU12205	U12205 Mycobacteri
16	20	100.0	5084	1	MSGRPOB	L27989 Mycobacteri
17	20	100.0	19352	1	AE006964	AE006964 Mycobacte
18	20	100.0	19770	1	MTCI376	Z95972 Mycobacteri
19	19	95.0	306	1	AF057493	AF057493 Mycobacte
20	19	95.0	306	6	AR157045	AR157045 Sequence
21	18.4	92.0	25	6	A47816	A47816 Sequence 30
22	18.4	92.0	306	1	AF057456	AF057456 Mycobacte
23	18.4	92.0	306	1	AF057459	AF057459 Mycobacte
24	18.4	92.0	306	1	AF057460	AF057460 Mycobacte
25	18.4	92.0	306	1	AF057471	AF057471 Mycobacte
26	18.4	92.0	306	1	AF057473	AF057473 Mycobacte
27	18.4	92.0	306	1	AF057496	AF057496 Corynebac
28	18.4	92.0	306	1	AF173087	AF173087 Mycobacte
29	18.4	92.0	306	6	AR157005	AR157005 Sequence
30	18.4	92.0	306	6	AR157010	AR157010 Sequence
31	18.4	92.0	306	6	AR157011	AR157011 Sequence
32	18.4	92.0	306	6	AR157021	AR157021 Sequence
33	18.4	92.0	306	6	AR157024	AR157024 Sequence
34	18.4	92.0	306	6	AR157046	AR157046 Sequence
c 35	18	90.0	87	6	AX050338	AX050338 Sequence
36	17.4	87.0	306	1	AF057463	AF057463 Mycobacte
37	17.4	87.0	306	1	AF057466	AF057466 Mycobacte
38	17.4	87.0	306	1	AF057475	AF057475 Mycobacte
39	17.4	87.0	306	1	AF057480	AF057480 Mycobacte
40	17.4	87.0	306	1	AF057489	AF057489 Mycobacte
41	17.4	87.0	306	1	AF057492	AF057492 Mycobacte
42	17.4	87.0	306	1	AF057494	AF057494 Rhodococc
43	17.4	87.0	306	1	AF057495	AF057495 Nocardia
44	17.4	87.0	306	1	AF173084	AF173084 Mycobacte
45	17.4	87.0	306	1	AF173086	AF173086 Mycobacte

ALIGNMENTS

RESULT 1
AF057450
LOCUS AF057450 306 bp DNA linear BCT 17-SEP-1999
DEFINITION Mycobacterium africanum RNA polymerase beta (rpoB) gene, partial cds.
ACCESSION AF057450
VERSION AF057450.1 GI:5902487
KEYWORDS .
SOURCE Mycobacterium africanum.
ORGANISM Mycobacterium africanum
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T., Kim,E.C., Cha,C.Y. and Kook,Y.H.
TITLE Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)
JOURNAL J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
MEDLINE 99262756
PUBMED 10325313
REFERENCE 2 (bases 1 to 306)
AUTHORS Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,

```
          Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE   Direct Submission
  JOURNAL Submitted (06-APR-1998) Microbiology, Seoul National University
          College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
          Korea
FEATURES             Location/Qualifiers
     source          1. .306
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                     /strain="ATCC25420"
                     /db_xref="ATCC:25420"
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     CDS             <1. .>306
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                     /db_xref="GI:5902488"
                     /translation="RTVGELIQNQIRVGMSRMERVVRERMTTQDVEAITPQTLINIRP
                     VVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDVHPSH"
BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


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Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   2
AF057451
LOCUS       AF057451                306 bp    DNA     linear   BCT 17-SEP-1999
DEFINITION  Mycobacterium bovis RNA polymerase beta (rpoB) gene, partial cds.
ACCESSION   AF057451
VERSION     AF057451.1  GI:5902489
KEYWORDS    .
SOURCE      Mycobacterium bovis.
  ORGANISM  Mycobacterium bovis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
  MEDLINE   99262756
   PUBMED   10325313
REFERENCE   2  (bases 1 to 306)
  AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
     source          1. .306
                     /organism="Mycobacterium bovis"
                     /strain="ATCC19210"
                     /db_xref="ATCC:19210"
                     /db_xref="taxon:1765"
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                     /gene="rpoB"
     CDS             <1. .>306
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                     /transl_table=11
                     /product="RNA polymerase beta"
                     /protein_id="AAD55515.1"
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                     /translation="RTVGELIQNQIRVGMSRMERVVRERMTTQDVEAITPQTLINIRP
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BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


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Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   3
AF057452
LOCUS       AF057452                306 bp    DNA     linear   BCT 17-SEP-1999
DEFINITION  Mycobacterium bovis BCG strain French 1173P2 RNA polymerase beta
            (rpoB) gene, partial cds.
ACCESSION   AF057452
VERSION     AF057452.1  GI:5902491
KEYWORDS    .
SOURCE      Mycobacterium bovis BCG.
  ORGANISM  Mycobacterium bovis BCG
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
  MEDLINE   99262756
   PUBMED   10325313
REFERENCE   2  (bases 1 to 306)
  AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
     source          1. .306
                     /organism="Mycobacterium bovis BCG"
                     /strain="French 1173P2"
                     /db_xref="taxon:33892"
     gene            <1. .>306
                     /gene="rpoB"
     CDS             <1. .>306
                     /gene="rpoB"
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                     /transl_table=11
                     /product="RNA polymerase beta"
                     /protein_id="AAD55516.1"
                     /db_xref="GI:5902492"
                     /translation="RTVGELIQNQIRVGMSRMERVVRERMTTQDVEAITPQTLINIRP
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BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


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Qy      1 tacggtcggcgagctgatcc 20
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Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   4
AF057453
LOCUS       AF057453                306 bp    DNA     linear   BCT 17-SEP-1999
DEFINITION  Mycobacterium bovis BCG RNA polymerase beta (rpoB) gene, partial
            cds.
ACCESSION   AF057453
VERSION     AF057453.1  GI:5902493
KEYWORDS    .
SOURCE      Mycobacterium bovis BCG.
  ORGANISM  Mycobacterium bovis BCG
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
  MEDLINE   99262756
   PUBMED   10325313
REFERENCE   2  (bases 1 to 306)
  AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
     source          1. .306
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                     /strain="Tokyo T172"
                     /db_xref="taxon:33892"
     gene            <1. .>306
                     /gene="rpoB"
     CDS             <1. .>306
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                     /transl_table=11
                     /product="RNA polymerase beta"
                     /protein_id="AAD55517.1"
                     /db_xref="GI:5902494"
                     /translation="RTVGELIQNQIRVGMSRMERVVRERMTTQDVEAITPQTLINIRP
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BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


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  Best Local Similarity  100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   5
AF057454
LOCUS       AF057454                306 bp    DNA     linear   BCT 08-OCT-1999
DEFINITION  Mycobacterium tuberculosis RNA polymerase beta (rpoB) gene, partial
            cds.
ACCESSION   AF057454
VERSION     AF057454.1  GI:5902495
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
  MEDLINE   99262756
   PUBMED   10325313
REFERENCE   2  (bases 1 to 306)
  AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
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                     /organism="Mycobacterium tuberculosis"
                     /strain="H37Rv; ATCC27294"
                     /db_xref="ATCC:27294"
                     /db_xref="taxon:1773"
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                     /gene="rpoB"
     CDS             <1. .>306
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                     /transl_table=11
                     /product="RNA polymerase beta"
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BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


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Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   6
AR157003
LOCUS       AR157003                306 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6242584.
ACCESSION   AR157003
VERSION     AR157003.1  GI:15125707
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kook,Y. and Kim,B.
  TITLE     Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
  JOURNAL   Patent: US 6242584-A 2 05-JUN-2001;
FEATURES             Location/Qualifiers
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BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


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  Best Local Similarity  100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
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Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   7
AR157007
LOCUS       AR157007                306 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 6 from patent US 6242584.
ACCESSION   AR157007
VERSION     AR157007.1  GI:15125711
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kook,Y.-H. and Kim,B.-J.
  TITLE     Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
  JOURNAL   Patent: US 6242584-A 6 05-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .306
                     /organism="unknown"
BASE COUNT       56 a     96 c    107 g     47 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 6;  Length 306;
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
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Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   8
AR157008
LOCUS       AR157008                306 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 7 from patent US 6242584.
ACCESSION   AR157008
VERSION     AR157008.1  GI:15125712
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kook,Y. and Kim,B.
  TITLE     Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
  JOURNAL   Patent: US 6242584-A 7 05-JUN-2001;
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BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   9
AR157042
LOCUS       AR157042                306 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 41 from patent US 6242584.
ACCESSION   AR157042
VERSION     AR157042.1  GI:15125746
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kook,Y. and Kim,B.
  TITLE     Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
  JOURNAL   Patent: US 6242584-A 41 05-JUN-2001;
FEATURES             Location/Qualifiers
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BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
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Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT  10
AR157051
LOCUS       AR157051                306 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 50 from patent US 6242584.
ACCESSION   AR157051
VERSION     AR157051.1  GI:15125755
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kook,Y. and Kim,B.
  TITLE     Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
  JOURNAL   Patent: US 6242584-A 50 05-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .306
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BASE COUNT       56 a     94 c    108 g     48 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 6;  Length 306;
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
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Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT  11
MSGRIFRNAP
LOCUS       MSGRIFRNAP              432 bp    DNA     linear   BCT 21-MAY-1993
DEFINITION  Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin
            resistance gene, complete cds.
ACCESSION   L05910
VERSION     L05910.1  GI:149991
KEYWORDS    RNA polymerase beta-subunit; rifampicin resistance.
SOURCE      Mycobacterium tuberculosis (strain H37) DNA.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 432)
  AUTHORS   Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T.,
            Colston,J., Matter,L., Schopfer,K. and Bodmer,T.
  TITLE     Detection of rifampicin-resistance mutation in Mycobacterium
            tuberculosis
  JOURNAL   Antimicrob. Agents Chemother. 341, 647-650 (1993)
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FEATURES             Location/Qualifiers
     source          1. .432
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     variation       149
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                     mutation 234 G"
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     variation       188
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                     /replace="c"
     variation       191
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                     mutation 203 T"
                     /replace="c"
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BASE COUNT       77 a    140 c    148 g     67 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 1;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 94;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db     18 TACGGTCGGCGAGCTGATCC 37
```

```
RESULT  12
AR067448
LOCUS       AR067448                 432 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 59 from patent US 5851763.
ACCESSION   AR067448
VERSION     AR067448.1  GI:5998670
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 432)
  AUTHORS   Heym,B., Cole,S., Young,D., Zhang,Y., Honore,N., Telenti,A. and
            Bodmer,T.
  TITLE     Rapid detection of antibiotic resistance in mycobacterium
            tuberculosis
  JOURNAL   Patent: US 5851763-A 59 22-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .432
                     /organism="unknown"
BASE COUNT       77 a    139 c    149 g     67 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 6;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 94;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db     18 TACGGTCGGCGAGCTGATCC 37


RESULT  13
I50706
LOCUS       I50706                   970 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1 from patent US 5643723.
ACCESSION   I50706
VERSION     I50706.1  GI:2472409
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 970)
  AUTHORS   Persing,D.H., Hunt,J.J., Young,K.K.Y., Felmlee,T.A., Roberts,G.D.
            and Whelan,A.Christian.
  TITLE     Detection of a genetic locus encoding resistance to rifampin in
            mycobacterial cultures and in clinical specimens
  JOURNAL   Patent: US 5643723-A 1 01-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .970
                     /organism="unknown"
BASE COUNT      182 a    302 c    330 g    156 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 6;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db    261 TACGGTCGGCGAGCTGATCC 280


RESULT  14
AX111339
LOCUS       AX111339                3534 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 2072 from Patent WO0123604.
ACCESSION   AX111339
VERSION     AX111339.1  GI:13927631
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
```

```
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 3534)
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 2072 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .3534
                     /organism="Mycobacterium tuberculosis"
                     /strain="Rv"
                     /db_xref="taxon:1773"
BASE COUNT      679 a   1081 c   1188 g    586 t
ORIGIN
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Query Match 100.0%; Score 20; DB 6; Length 3534;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 tacggtcggcgagctgatcc 20
           ||||||||||||||||||||
Db    1137 TACGGTCGGCGAGCTGATCC 1156
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```
RESULT  15
MTU12205
LOCUS       MTU12205                3853 bp    DNA     linear   BCT 02-MAR-2000
DEFINITION  Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
            gene, partial cds.
ACCESSION   U12205
VERSION     U12205.1  GI:515684
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 3853)
  AUTHORS   Imboden,P., Troller,R., Marchesi,F., Telenti,A., Bodmer,T.,
            Cole,S., Schopfer,K. and Burkart,T.
  TITLE     The rpoB gene of Mycobacterium tuberculosis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3853)
  AUTHORS   Imboden,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-1994) Paul Imboden, Institute for Medical
            Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
            3010, Switzerland
FEATURES             Location/Qualifiers
     source          1. .3853
                     /organism="Mycobacterium tuberculosis"
                     /strain="H37Rv"
                     /db_xref="taxon:1773"
     gene            576. .>3853
                     /gene="rpoB"
     CDS             576. .>3853
                     /gene="rpoB"
                     /codon_start=1
                     /transl_table=11
                     /product="RNA-polymerase beta subunit"
                     /protein_id="AAA20242.2"
                     /db_xref="GI:7144499"
                     /translation="MLEGCILADSRQSKTAASPSPSRPQSSSNNSVPGAPNRVSFAKL
                     REPLEVPGLLDVQTDSFEWLIGSPRWRESAAERGDVNPVGGLEEVLYELSPIEDFSGS
                     MSLSFSDPRFDDVKAPVDECKDKDMTYAAPLFVTAEFINNNTGEIKSQTVFMGDFPMM
                     TEKGTFIINGTERVVVSQLVRSPGVYFDETIDKSTDKTLHSVKVIPSRGAWLEFDVDK
                     RDTVGVRIDRKRRQPVTVLLKALGWTSEQIVERFGFSEIMRSTLEKDNTVGTDEALLD
                     IYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARVGRYKVNKKLGLHVGEPITSSTLT
                     EEDVVATIEYLVRLHEGQTTMTVPGGVEVPVETDDIDHFGNRRLRTVGELIQNQIRVG
                     MSRMERVVRERMTTQDVEAITPQTLINIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLT
                     HKRRLSALGPGGLSRERAGLEVRDVHPSHYGRMCPIETPEGPNIGLIGSLSVYARVNP
                     FGFIETPYRKVVDGVVSDGIVYLTADEEDRHVVAQANSPIDADGRFVEPRVLVRRKAG
                     EVEYVPSSEVDYMDVSPRQMVSVATAMIPFLEHDDANRALMGANMQRQAVPLVRSEAP
                     LVGTGMELRAAIDAATSSSQESGVIEEVSADYITVMHDNGTRRTYRMRKFARSNHGTC
                     ANQCPIVDAGDRVEAGQVIADGPCTDDGEMALGKNLLVAIMPWEGHNYEDAIILSNRL
                     VEEDVLTSIHIEEHEIDARDTKLGAEEITRDIPNISDEVLADLDERGIVRIGAEVRDG
                     DILVGKVTPKGETELTPEERLLRAIFGEKAREVRDTSLKVPHGESGKVIGIRVFSRED
                     EDELPAGVNELVRVYVAQKRKISDGDKLAGRHGNKGVIGKILPVEDMPFLADGTPVDI
                     ILNTHGVPRRMNIGQILETHLGWCAHSGWKVDAAKGVPDWAARLPDELLEAQPNAIVS
                     TPVFDGAQEAELQGLLSCTLPNRDGDVLVDADGKAMLFDGRSGEPFPYPVTVGYMYIM
                     KLHHLVDDKIHARSTGPYSMITQQPLGGKAQFGGQRFGEMECWAMQAYGAAYTLQELL
                     TIKS"
BASE COUNT      723 a   1173 c   1293 g    664 t
ORIGIN
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Query Match 100.0%; Score 20; DB 1; Length 3853;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 tacggtcggcgagctgatcc 20
           ||||||||||||||||||||
Db    1712 TACGGTCGGCGAGCTGATCC 1731
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Search completed: August 7, 2002, 21:51:38
Job time: 23873 sec

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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:15:17 ; Search time 4103.44 Seconds
(without alignments)
65.784 Million cell updates/sec

Title: US-09-786-105-2
Perfect score: 20
Sequence: 1 tacggcgtttcgatgaaccc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17.4	87.0	396	10	BF220419	BF220419 NXCI_146_
2	17.4	87.0	399	10	BF169611	BF169611 NXCI_125_
3	17.4	87.0	452	10	BG040291	BG040291 NXSI_110_
4	17.4	87.0	539	9	AA556698	AA556698 553 Loblo
5	17.4	87.0	545	10	BF777209	BF777209 NXSI_066_
c 6	17	85.0	234	10	W06754	W06754 SMEST0390 S
c 7	17	85.0	579	10	T24127	T24127 SMEST0325 S
8	16.8	84.0	277	9	AA734164	AA734164 vs19g12.r
c 9	16.4	82.0	576	10	BF252921	BF252921 EST420184
10	16.4	82.0	624	10	BE896357	BE896357 601439015
11	16.4	82.0	631	12	BH615799	BH615799 BMBAC304F
c 12	16.4	82.0	961	12	AG141490	AG141490 Pan trogl
c 13	15.8	79.0	213	9	AW064407	AW064407 SP0996 KR
14	15.8	79.0	436	9	AI496312	AI496312 sb05b08.y
c 15	15.8	79.0	582	12	CNS01K68	AL147937 Anopheles
16	15.8	79.0	637	10	BG908684	BG908684 TaLr1170D
17	15.8	79.0	650	10	BG908616	BG908616 TaLr1169H
c 18	15.8	79.0	752	12	CNS03678	AL229661 Tetraodon
c 19	15.8	79.0	775	12	AZ125549	AZ125549 OSJNBb009
c 20	15.8	79.0	885	12	CNS02B0Q	AL189251 Tetraodon
c 21	15.8	79.0	913	10	BF204833	BF204833 601867133
c 22	15.8	79.0	1029	12	CNS0549K	AL320465 Tetraodon
c 23	15.8	79.0	1411	10	BI663170	BI663170 603286791
c 24	15.6	78.0	885	12	CNS01K02	AL147715 Anopheles
25	15.4	77.0	248	10	BG140300	BG140300 EST480742
c 26	15.4	77.0	269	9	AV640876	AV640876 AV640876
27	15.4	77.0	384	10	BM077908	BM077908 pb21g06.y
c 28	15.4	77.0	390	9	AV644609	AV644609 AV644609
29	15.4	77.0	467	12	CNS03FUV	AL242176 Tetraodon
c 30	15.4	77.0	474	9	AV396989	AV396989 AV396989
31	15.4	77.0	489	9	AW618736	AW618736 EST320722
c 32	15.4	77.0	497	9	AV643117	AV643117 AV643117
c 33	15.4	77.0	508	9	AV642711	AV642711 AV642711
c 34	15.4	77.0	518	9	AV642141	AV642141 AV642141
c 35	15.4	77.0	531	9	AV642766	AV642766 AV642766
36	15.4	77.0	532	10	BI506216	BI506216 BB170018A
37	15.4	77.0	536	12	AQ783856	AQ783856 HS_2001_A
38	15.4	77.0	548	12	AQ497017	AQ497017 HS_5197_B
c 39	15.4	77.0	566	9	AV631818	AV631818 AV631818
40	15.4	77.0	788	10	BE566696	BE566696 601339653
41	15.2	76.0	146	10	BM096759	BM096759 EBma07_SQ
42	15.2	76.0	200	10	BM098906	BM098906 EBpi05_SQ
43	15.2	76.0	205	12	AZ577000	AZ577000 06d05 Sho
44	15.2	76.0	269	10	BF953380	BF953380 RC3-NN019
45	15.2	76.0	317	9	BB501888	BB501888 BB501888

ALIGNMENTS

RESULT 1
BF220419
LOCUS BF220419 396 bp mRNA linear EST 08-NOV-2000
DEFINITION NXCI_146_A06_F NXCI (Nsf Xylem Compression wood Inclined) Pinus taeda cDNA clone NXCI_146_A06 5', mRNA sequence.
ACCESSION BF220419
VERSION BF220419.1 GI:11126551
KEYWORDS EST.
SOURCE loblolly pine.
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 396)
AUTHORS Sederoff,R.
TITLE Molecular Basis of Wood Formation in the Pine Megagenome
JOURNAL Unpublished (2000)
COMMENT Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .396
/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NXCI_146_A06"
/clone_lib="NXCI (Nsf Xylem Compression wood Inclined)"
/tissue_type="Xylem"
/cell_type="Compression"
/dev_stage="Juvenile"
/lab_host="XL1-Blue"
/note="Vector: BlueScript SK; Site_1: Eco RI; Site_2: XhoI ; The library is from early (spring) wood, taken from three six-year old trees (three different genotypes), in the juvenile phase. These trees were induced to form compression wood by bending to a 45 degree angle and tying them to the ground. Differentiating xylem was harvested from the bottoms of the inclined stems, and a mixture of

all three genotypes was used for the library. oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI BlueScript SK vector arms. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGCACGAG'."
BASE COUNT 71 a 84 c 122 g 110 t 9 others
ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 396;
Best Local Similarity 94.7%; Pred. No. 71;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 acggcgtttcgatgaaccc 20
|||||| ||||||||||||
Db 15 ACGGCGCTTCGATGAACCC 33

RESULT 2
BF169611
LOCUS BF169611 399 bp mRNA linear EST 30-OCT-2000
DEFINITION NXCI_125_C05_F NXCI (Nsf Xylem Compression wood Inclined) Pinus taeda cDNA clone NXCI_125_C05 5', mRNA sequence.
ACCESSION BF169611
VERSION BF169611.1 GI:11054228
KEYWORDS EST.
SOURCE loblolly pine.
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 399)
AUTHORS Sederoff,R.
TITLE Molecular Basis of Wood Formation in the Pine Megagenome
JOURNAL Unpublished (2000)
COMMENT Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .399
/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NXCI_125_C05"
/clone_lib="NXCI (Nsf Xylem Compression wood Inclined)"
/tissue_type="Xylem"
/cell_type="Compression"
/dev_stage="Juvenile"
/lab_host="XL1-Blue"
/note="Vector: BlueScript SK; Site_1: Eco RI; Site_2: XhoI ; The library is from early (spring) wood, taken from three six-year old trees (three different genotypes), in the juvenile phase. These trees were induced to form compression wood by bending to a 45 degree angle and tying them to the ground. Differentiating xylem was harvested from the bottoms of the inclined stems, and a mixture of all three genotypes was used for the library. oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI BlueScript SK vector arms. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGCACGAG'."
BASE COUNT 71 a 84 c 121 g 121 t 2 others
ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 399;
Best Local Similarity 94.7%; Pred. No. 72;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 acggcgtttcgatgaaccc 20
|||||| ||||||||||||
Db 15 ACGGCGCTTCGATGAACCC 33

RESULT 3
BG040291
LOCUS BG040291 452 bp mRNA linear EST 24-JAN-2001
DEFINITION NXSI_110_F06_F NXSI (Nsf Xylem Side wood Inclined) Pinus taeda cDNA clone NXSI_110_F06 5', mRNA sequence.
ACCESSION BG040291
VERSION BG040291.1 GI:12482876
KEYWORDS EST.
SOURCE loblolly pine.
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 452)
AUTHORS Sederoff,R.
TITLE Molecular Basis of Wood Formation in the Pine Megagenome
JOURNAL Unpublished (2000)
COMMENT Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .452
/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NXSI_110_F06"
/clone_lib="NXSI (Nsf Xylem Side wood Inclined)"
/tissue_type="Xylem"
/cell_type="Side"
/dev_stage="Juvenile"
/lab_host="XL1-Blue"
/note="Vector: BlueScript SK; Site_1: Eco RI; Site_2: XhoI ; The library is from early (spring) wood, taken from three six-year old trees (three different genotypes), in the juvenile phase. These trees were induced to form side wood by bending to a 45 degree angle and tying them to the ground. Differentiating xylem was harvested from the sides of the inclined stems, and a mixture of all three genotypes was used for the library. oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI BlueScript SK vector arms. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGCACGAG'."
BASE COUNT 71 a 122 c 146 g 95 t 18 others
ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 452;
Best Local Similarity 94.7%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 acggcgtttcgatgaaccc 20
|||||| ||||||||||||
Db 329 ACGGCGCTTCGATGAACCC 347

RESULT 4
AA556698
LOCUS AA556698 539 bp mRNA linear EST 28-AUG-1998
DEFINITION 553 Loblolly pine CA Pinus taeda cDNA clone lCAB4G, mRNA sequence.
ACCESSION AA556698
VERSION AA556698.1 GI:3365713
KEYWORDS EST.
SOURCE loblolly pine.
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 539)

```
  AUTHORS   Allona,I., Quinn,M., Shoop,E., Swope,K., St.Cyr,S., Carlis,J.,
            Riedl,J., Retzel,E, Campbell,M.M., Sederoff,R. and Whetten,R.W.
  TITLE     Analysis of xylem formation in pine by cDNA sequencing
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 95 (16), 9693-9698 (1998)
  MEDLINE   98356220
COMMENT     Contact: Ross Whetten
            Forest Biotechnology Group
            North Carolina State University
            Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
            ,NC, 27695-8008
            Tel: 919-515-7800
            Fax: 919-515-7801
            Email: rosswhet@unity.ncsu.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .539
                     /organism="Pinus taeda"
                     /strain="Coastal plain loblolly pine from North Carolina"
                     /db_xref="taxon:3352"
                     /clone="1CAB4G"
                     /clone_lib="Loblolly pine CA"
                     /tissue_type="Xylem"
                     /lab_host="SOLR"
                     /note="Vector: lambda-ZAP; Site_1: EcoRI; Site_2: XhoI;
                     The result of subtraction of C library with N library.
                     Immature xylem from the underside of inclined stems of
                     differentiating compression wood was subtracted with
                     immature xylem from the side of inclined stems of
                     differentiating wood. A mixture of four genotypes were
                     used. Oligo-dT primed cDNA was directionally cloned into
                     the EcoRI-XhoI lambda-ZAP vector arms"
BASE COUNT      102 a    120 c    156 g    150 t     11 others
ORIGIN


  Query Match             87.0%;  Score 17.4;  DB 9;  Length 539;
  Best Local Similarity   94.7%;  Pred. No. 78;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 acggcgtttcgatgaaccc 20
          |||||| ||||||||||||
Db    145 ACGGCGCTTCGATGAACCC 163


RESULT   5
BF777209
LOCUS       BF777209                545 bp    mRNA    linear   EST 12-JAN-2001
DEFINITION  NXSI_066_E05_F NXSI (Nsf Xylem Side wood Inclined) Pinus taeda cDNA
            clone NXSI_066_E05 5', mRNA sequence.
ACCESSION   BF777209
VERSION     BF777209.1  GI:12125109
KEYWORDS    EST.
SOURCE      loblolly pine.
  ORGANISM  Pinus taeda
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE   1  (bases 1 to 545)
  AUTHORS   Sederoff,R.
  TITLE     Molecular Basis of Wood Formation in the Pine Megagenome
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Johnson, Arthur
            North Carolina State University
            Tel: 919 515 7800
            Fax: 919 515 7801
            Email: ajohnson@unity.ncsu.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .545
                     /organism="Pinus taeda"
                     /strain="Coastal plain loblolly pine from North Carolina"
                     /db_xref="taxon:3352"
                     /clone="NXSI_066_E05"
                     /clone_lib="NXSI (Nsf Xylem Side wood Inclined)"
                     /tissue_type="Xylem"
                     /cell_type="Side"
                     /dev_stage="Juvenile"
                     /lab_host="XL1-Blue"
                     /note="Vector: BlueScript SK; Site_1: Eco RI; Site_2: XhoI
                     ; The library is from early (spring) wood, taken from
                     three six-year old trees (three different genotypes), in
                     the juvenile phase. These trees were induced to form side
                     wood by bending to a 45 degree angle and tying them to the
                     ground. Differentiating xylem was harvested from the sides
                     of the inclined stems, and a mixture of all three
                     genotypes was used for the library. oligo-dT primed cDNA
                     was directionally cloned into the EcoRI-XhoI BlueScript SK
                     vector arms. NOTE: The sequences contain a 'cDNA adapter'
                     between the EcoRI site and the start of the EST. The
                     adapter sequence is 'AATTCGGCACGAG'."
BASE COUNT      92 a    142 c    167 g    132 t     12 others
ORIGIN


  Query Match             87.0%;  Score 17.4;  DB 10;  Length 545;
  Best Local Similarity   94.7%;  Pred. No. 78;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 acggcgtttcgatgaaccc 20
          |||||| ||||||||||||
Db    256 ACGGCGCTTCGATGAACCC 274


RESULT   6
W06754/c
LOCUS       W06754                  234 bp    mRNA    linear   EST 01-JUL-1996
DEFINITION  SMEST0390 Schistosoma mansoni, adult worm, Gloria Franco
            Schistosoma mansoni cDNA clone SMPBE73 3' end, mRNA sequence.
ACCESSION   W06754
VERSION     W06754.1  GI:1444974
KEYWORDS    EST.
SOURCE      Schistosoma mansoni.
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 234)
  AUTHORS   Franco,G.R. and Pena,S.D.J.
  TITLE     Franco,G.R. and Pena,S.D.J., Unpublished
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Franco G.R. and Pena S.D.J.
            Laboratorio de Genetica-Bioquimica, Departamento de Bioquimicae
            Imunologia
            Instituto de Ciencias Biologicas, Universidade Federal de Minas
            Gerais
            Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
            Tel: (5531)4415611
            Fax: (5531)4415409
            Email: gfranco@mono.icb.ufmg.br
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .234
                     /organism="Schistosoma mansoni"
                     /strain="NMRI"
                     /db_xref="taxon:6183"
                     /clone="SMPBE73"
                     /clone_lib="Schistosoma mansoni, adult worm, Gloria
                     Franco"
                     /lab_host="DH10B, JM109"
                     /note="Vector: BA vector; Site_1: NotI; Site_2: HindIII;
                     Total cellular RNA from male and female adult worms was
                     extracted  according to a modification (Puissant, C. and
                     Houdebine, L. M.  BioFeedback 8, 148-149, 1990) of the
                     Guanidine Thiocyanate  procedure (Chomczynski, P. and
                     Sacchi, N. Anal. Biochem. 162, 156- 159, 1987). Poly (A)+
                     RNA was purified by oligo dT column and cDNA  was
                     synthesized as described previously (Adams, M. D. et al.
                     Nature  Genet. 4, 373-389, 1993). cDNA was ligated to a
```

two fold molar excess of a NotI/HindIII digested plasmid DNA (lafmid BA vector, a phagemid derived from pEMBL, Adams, M. D. et al. Nature Genet. 4, 373-389, 1993)) and electroporated into E. coli strain DH10B (BRL). The library was amplified and further selected for clones containing long inserts (>500 bp) by purification of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel, containing the smear of the library and electroporation into DH10B cells. "

BASE COUNT 49 a 84 c 66 g 33 t 2 others
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 234;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaa 17
||||||||||||||||||
Db 64 TACGGCGTTTCGATGAA 48

RESULT 7
T24127/c
LOCUS T24127 579 bp mRNA linear EST 27-FEB-1995
DEFINITION SMEST0325 Schistosoma mansoni, adult worm, Gloria Franco Schistosoma mansoni cDNA clone SMPBC65 3', mRNA sequence.
ACCESSION T24127
VERSION T24127.1 GI:529730
KEYWORDS EST.
SOURCE Schistosoma mansoni.
ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE 1 (bases 1 to 579)
AUTHORS Franco,G.R., Adams,M.D., Soares,M.B., Simpson,A.J.G., Venter,J.C. and Pena,S.D.J.
TITLE Identification of new Schistosoma mansoni genes by the EST strategy using a directional cDNA library
JOURNAL Gene 152, 141-147 (1995)
MEDLINE 95137379
COMMENT Contact: Franco G.R. and Pena S.D.J.
Laboratorio de Genetica-Bioquimica, Departamento de Bioquimicae Imunologia
Instituto de Ciencias Biologicas, Universidade Federal de Minas Gerais
Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
Tel: (5531)4415611
Fax: (5531)4415409
Email: gfranco@mono.icb.ufmg.br
Seq primer: M13 Forward.
FEATURES Location/Qualifiers
source 1. .579
/organism="Schistosoma mansoni"
/strain="NMRI"
/db_xref="taxon:6183"
/clone="SMPBC65"
/clone_lib="Schistosoma mansoni, adult worm, Gloria Franco"
/lab_host="DH10B, JM109"
/note="Vector: BA vector; Site_1: NotI; Site_2: HindIII; Total cellular RNA from male and female adult worms was extracted according to a modification (Puissant, C. and Houdebine, L. M. BioFeedback 8, 148-149, 1990) of the Guanidine Thiocyanate procedure (Chomczynski, P. and Sacchi, N. Anal. Biochem. 162, 156- 159, 1987). Poly (A)+ RNA was purified by oligo dT column and cDNA was synthesized as described previously (Adams, M. D. et al. Nature Genet. 4, 373-389, 1993). cDNA was ligated to a two fold molar excess of a NotI/HindIII digested plasmid DNA (lafmid BA vector, a phagemid derived from pEMBL, Adams, M. D. et al. Nature Genet. 4, 373-389, 1993)) and electroporated into E. coli strain DH10B (BRL). The library was amplified and further selected for clones containing long inserts (>500 bp) by purification of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel, containing the smear of the library and electroporation into DH10B cells. "

BASE COUNT 102 a 206 c 179 g 88 t 4 others
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaa 17
||||||||||||||||||
Db 75 TACGGCGTTTCGATGAA 59

RESULT 8
AA734164
LOCUS AA734164 277 bp mRNA linear EST 07-JAN-1998
DEFINITION vs19g12.r1 Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone IMAGE:1138726 5' similar to gb:X80699 M.musculus L26 mRNA (MOUSE);, mRNA sequence.
ACCESSION AA734164
VERSION AA734164.1 GI:2755831
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 277)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:619998
Trace considered overall poor quality
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .277
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:1138726"
/clone_lib="Barstead mouse irradiated colon MPLRB7"
/dev_stage="8 weeks"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; Tissue obtained from 8 week old mouse. Colon was harvested 72 hours after irradiation with 1400 Gys. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'TGTTACGAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead. "
BASE COUNT 64 a 59 c 92 g 62 t
ORIGIN

```
  Query Match            84.0%;  Score 16.8;  DB 9;  Length 277;
  Best Local Similarity  90.0%;  Pred. No. 1.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          |||||| |||||||| ||||
Db     47 TACGGCATTTCGATGCACCC 66


RESULT   9
BF252921/c
LOCUS       BF252921                576 bp    mRNA    linear   EST 15-NOV-2001
DEFINITION  EST420184 Coccidioides immitis spherule cDNA library Coccidioides
            immitis cDNA clone CIABC49 5' sequence, mRNA sequence.
ACCESSION   BF252921
VERSION     BF252921.1  GI:16933064
KEYWORDS    EST.
SOURCE      Coccidioides immitis.
  ORGANISM  Coccidioides immitis
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE   1  (bases 1 to 576)
  AUTHORS   Gardner,M.J. and Kirkland,T.
  TITLE     Generation of ESTs from Coccidioides immitis spherule cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Malcolm J. Gardner
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org.
FEATURES             Location/Qualifiers
     source          1. .576
                     /organism="Coccidioides immitis"
                     /db_xref="taxon:5501"
                     /clone="CIABC49"
                     /clone_lib="Coccidioides immitis spherule cDNA library"
                     /dev_stage="spherule"
                     /lab_host="SOLR"
                     /note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2:
                     Xho1"
BASE COUNT      113 a    186 c    176 g    101 t
ORIGIN


  Query Match            82.0%;  Score 16.4;  DB 10;  Length 576;
  Best Local Similarity  94.4%;  Pred. No. 2.7e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 cggcgtttcgatgaaccc 20
          |||||| ||||||||||
Db    241 CGGCGTGTCGATGAACCC 224


RESULT  10
BE896357
LOCUS       BE896357                624 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601439015F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924266 5',
            mRNA sequence.
ACCESSION   BE896357
VERSION     BE896357.1  GI:10360678
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 624)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9761  row: m  column: 03
            High quality sequence start: 2
            High quality sequence stop: 403.
FEATURES             Location/Qualifiers
     source          1. .624
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3924266"
                     /clone_lib="NIH_MGC_72"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."
BASE COUNT      155 a    209 c    150 g    110 t
ORIGIN


  Query Match            82.0%;  Score 16.4;  DB 10;  Length 624;
  Best Local Similarity  94.4%;  Pred. No. 2.8e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 cggcgtttcgatgaaccc 20
          | ||||||||||||||||
Db    580 CCGCGTTTCGATGAACCC 597


RESULT  11
BH615799
LOCUS       BH615799                631 bp    DNA     linear   GSS 28-JAN-2002
DEFINITION  BMBAC304F01SP6_PSU Brugia malayi Genomic Bac Library 3 Brugia
            malayi genomic, DNA sequence.
ACCESSION   BH615799
VERSION     BH615799.1  GI:18380487
KEYWORDS    GSS.
SOURCE      Brugia malayi.
  ORGANISM  Brugia malayi
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Brugia.
REFERENCE   1  (bases 1 to 631)
  AUTHORS   Whitton,C., Daub,J., Ware,J., Quail,M., Hall,N., Barrell,B., Foster
            ,J., Guiliano,D., Slatko,B. and Blaxter,M.
  TITLE     Genome survey sequences from the human parasitic nematode Brugia
            malayi
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Blaxter ML
            Institute of Cell, Animal and Population Biology
            University of Edinburgh
            Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
            3JT, UK
            Tel: +44 131 650 6760
            Fax: +44 131 670 5450
            Email: mark.blaxter@ed.ac.uk
            Sequenced from the Brugia malayi BAC library constructed by Claire
            Whitton and Dr Mike Quail. The sequence was generated by The
            Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in
            collaboration with Mark Blaxter, ICAPB, University of Edinburgh,
            Edinburgh, UK.
            Seq primer: SP6 (ATTTAGGTGACACTATAG)
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .631
                     /organism="Brugia malayi"
```

```
                     /strain="TRS"
                     /db_xref="taxon:6279"
                     /clone_lib="Brugia malayi Genomic Bac Library 3"
                     /sex="Mixed (male and female)"
                     /tissue_type="whole parasite"
                     /dev_stage="microfilaria (L1)"
                     /note="Vector: pBACe3.6; Site_1: BamH I; Brugia malayi
                     genomic DNA was partially cleaved with Sau3A I and size
                     fractionated. 7,392 clones were generated with mean insert
                     size ~48 kbp. The library was constructed by Claire
                     Whitton, Blaxter Nematode Genetics Lab, University of
                     Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing
                     Unit, The Sanger Centre, Cambridge, UK."
BASE COUNT      196 a     94 c    142 g    199 t
ORIGIN


  Query Match             82.0%;  Score 16.4;  DB 12;  Length 631;
  Best Local Similarity   94.4%;  Pred. No. 2.8e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 acggcgtttcgatgaacc 19
          |||||||||||||||| ||
Db    606 ACGGCGTTTCGATGATCC 623


RESULT  12
AG141490/c
LOCUS       AG141490                961 bp    DNA     linear   GSS 08-JAN-2002
DEFINITION  Pan troglodytes DNA, clone: RP43-001J13.TJ, genomic survey
            sequence.
ACCESSION   AG141490
VERSION     AG141490.1  GI:16671168
KEYWORDS    GSS; GSS (genome survey sequence).
SOURCE      Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
            Male BAC Library clone:RP43-001J13.TJ.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (sites)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library RPCI-43
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 961)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
            end was generated during the R&D process and may have higher chance
            of clone tracking errors.
             PRIMERS
                 Sequencing: TJ
             LIBRARY
                 Vector    : pBACe3.6
                 R.Site 1  : EcoRI
                 R.Site 2  : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .961
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /clone="RP43-001J13.TJ"
                     /sex="male"
                     /cell_type="lymphocytes"
                     /clone_lib="RPCI-43 Chimpanzee Male BAC Library"
BASE COUNT      255 a    299 c    145 g    252 t     10 others
ORIGIN


  Query Match             82.0%;  Score 16.4;  DB 12;  Length 961;
  Best Local Similarity   94.4%;  Pred. No. 3.1e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 acggcgtttcgatgaacc 19
          |||||||| |||||||||
Db    746 ACGGCGTTACGATGAACC 729


RESULT  13
AW064407/c
LOCUS       AW064407                213 bp    mRNA    linear   EST 07-DEC-2000
DEFINITION  SP0996 KRIBB Human CD4 intrathymic T-cell cDNA library Homo sapiens
            cDNA 3', mRNA sequence.
ACCESSION   AW064407
VERSION     AW064407.1  GI:8888344
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 213)
  AUTHORS   Goh,S.-H., Park,J.-H., Lee,Y.J., Lee,H.G., Yoo,H.-S., Lee,I.-C.,
            Park,J.-H., Kim,Y.-S. and Lee,C.-C.
  TITLE     Gene expression profile and identification of differentially
            expressed transcripts during human intrathymic T-cell development
            by cDNA sequencing analysis
  JOURNAL   Genomics 70 (1), 1-18 (2000)
  MEDLINE   20541704
COMMENT     Contact: Sung-Ho Goh
            Genome Center
            Korea Research Institute of Bioscience and Biotechnology
            Oun-dong 52, Yu Sung-Gu, Daejon 305-333, Republic of Korea
            Tel: 82-42-860-4473
            Fax: 82-42-860-4479
            Email: gohsh@mail.kribb.re.kr
            Seq primer: T7
            High quality sequence stop: 213
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .213
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="KRIBB Human CD4 intrathymic T-cell cDNA
                     library"
                     /tissue_type="Thymus"
                     /cell_type="Intrathymic T-cell"
                     /dev_stage="CD3+4+8- single positive stage"
                     /note="Vector: pGEM-T; cDNA was made from total
                     cytoplasmic RNA of sorted human intrathymic CD3+4+8-
                     T-cell, adaptor ligated, amplified with PCR, and cloned
                     into pGEM-T vector."
BASE COUNT       41 a     59 c     72 g     40 t      1 others
ORIGIN


  Query Match             79.0%;  Score 15.8;  DB 9;  Length 213;
  Best Local Similarity   89.5%;  Pred. No. 4.3e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 acggcgtttcgatgaaccc 20
          |||||| || |||||||||
Db     43 ACGGCGGTTTGATGAACCC 25


RESULT  14
AI496312
LOCUS       AI496312                436 bp    mRNA    linear   EST 30-NOV-2001
DEFINITION  sb05b08.y1 Gm-c1004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
            Gm-c1004-7888 5' similar to TR:Q92388 Q92388 CRG1 GENE. ;, mRNA
            sequence.
ACCESSION   AI496312
```

```
VERSION     AI496312.1  GI:4397315
KEYWORDS    EST.
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 436)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available through: ResGen, Invitrogen Corp. 2130
            South Memorial Parkway Huntsville, AL 35801 For further information
            call: (800)-533-4363 or contact via email: ccu@resgen.com
            Seq primer: -40RP from Gibco
            High quality sequence stop: 386
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .436
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
                     /clone="GENOME SYSTEMS CLONE ID: Gm-c1004-7888"
                     /clone_lib="Gm-c1004"
                     /tissue_type="root"
                     /lab_host="XL10-Gold"
                     /note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
                     XhoI; Root cDNA. The mRNA was isolated from entire roots
                     of 8 day old 'Williams' seedlings which were propagated on
                     paper towels with distilled water. Stratagene's  cDNA
                     Synthesis Kit (catalog #200401) was used to synthesize the
                     cDNA. First- strand synthesis was performed with 5-methyl
                     dCTP, hence the ligated cDNA is hemimethylated.
                     Stratagene's first-strand synthesis primer was used
                     [GAGAGAGAGAGAGAGAGAGAACTAGTCTCGAG(T)-18]. After
                     second-strand synthesis, the cDNA ends were 'polished'
                     with clone Pfu DNA polymerase, ligated to EcoRI adapters,
                     and phosphorylated. The XhoI site within the first-strand
                     synthesis primer was restricted by digestion with XhoI;
                     all XhoI sites in the  cDNA would be protected by their
                     hemimethylated status. The cDNA constructs were
                     size-fractionated with a 500bp cutoff, using GibcoBRL Life
                     Technologies' cDNA Size Fractionation column. The column
                     eluent was then ligated into  Stratagene's pBluescript II
                     XR Predigested vector (pBluescript II SK(+) that had been
                     digested with EcoRI and XhoI, and phosphorylated). Both
                     the white  and blue colonies appear to contain recombinant
                     plasmids with cDNA inserts. Blue colonies 9n=15) have been
                     sequenced, and possess putative cDNA inserts. This library
                     was constructed by Dr. Paul Keim & Virginia H. Coryell,
                     Department of Biology, Box5640, Northern Arizona
                     University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr.
                     Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax:
                     520-523-7500, email: paul.keim@nau.edu,
                     virginia.coryell@nau.edu"
BASE COUNT       90 a    174 c     96 g     76 t
ORIGIN


  Query Match            79.0%;  Score 15.8;  DB 9;  Length 436;
  Best Local Similarity  89.5%;  Pred. No. 5.3e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 acggcgtttcgatgaaccc 20
           ||| ||| ||||||||||| 
Db     185 ACGCCGTCTCGATGAACCC 203


RESULT 15
CNS01K68/c
LOCUS       CNS01K68                582 bp    DNA     linear   GSS 12-JUN-2001
DEFINITION  Anopheles gambiae GSS SP6 end of clone 16E18 of NotreDame1 library
            from strain PEST of Anopheles gambiae (African malaria mosquito),
            genomic survey sequence.
ACCESSION   AL147937
VERSION     AL147937.1  GI:7006083
KEYWORDS    GSS.
SOURCE      African malaria mosquito.
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
            Culicoidea; Anopheles.
REFERENCE   1  (bases 1 to 582)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
REFERENCE   2  (bases 1 to 582)
  AUTHORS   Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
            Roux, Paris 75015, France
COMMENT     This clone is from an A. gambiae BAC library provided by F.H.
            Collins and sequenced by Genoscope in collaboration with the
            Laboratory of Biochem. and Biol. Molec. of Insects, Institut
            Pasteur.
FEATURES             Location/Qualifiers
     source          1. .582
                     /organism="Anopheles gambiae"
                     /strain="PEST"
                     /db_xref="taxon:7165"
                     /clone="16E18"
                     /clone_lib="NotreDame1"
                     /note="end : SP6"
BASE COUNT      160 a    124 c    136 g    153 t      9 others
ORIGIN


  Query Match            79.0%;  Score 15.8;  DB 12;  Length 582;
  Best Local Similarity  89.5%;  Pred. No. 5.7e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 acggcgtttcgatgaaccc 20
           |||||||||||||| | ||
Db     320 ACGGCGTTTCGATGTAGCC 302


Search completed: August  7, 2002, 21:15:20
Job time: 22890 sec
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 22:03:58 ; Search time 568.44 Seconds
(without alignments)
60.408 Million cell updates/sec

Title: US-09-786-105-2
Perfect score: 20
Sequence: 1 tacggcgtttcgatgaaccc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*
1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	21	AAA49824	Mycobacterium tube
	2	20	100.0	20	21	AAA49826	Mycobacterium tube
c	3	20	100.0	432	14	AAQ61457	M.tuberculosis rpo
c	4	20	100.0	480	21	AAA49863	Mycobacterium tube
c	5	20	100.0	620	17	AAT29126	rpoB gene fragment
c	6	20	100.0	620	17	AAT29124	rpoB gene fragment
c	7	20	100.0	620	17	AAT29125	rpoB gene fragment
c	8	20	100.0	970	17	AAT09676	Mycobacterium tube
c	9	20	100.0	3519	22	AAH51976	Mycobacterium tube
c	10	20	100.0	3534	22	AAH02079	Mycobacterium tube
c	11	20	100.0	3853	21	AAA74651	Mycobacterium tube
c	12	20	100.0	3853	21	AAA89994	M. tuberculosis rp
	13	19	95.0	19	17	AAT12096	M. tuberculosis rp
c	14	18.4	92.0	3447	14	AAQ51532	M.leprae rpoB gene
c	15	16.8	84.0	3474	23	AAS51357	Enterococcus faeca
c	16	16.8	84.0	3624	23	AAS52892	Enterococcus faeca
	17	16.8	84.0	9179	20	AAX13246	Enterococcus faeca
c	18	15.4	77.0	612	22	AAF71082	C. glutamicum SRT
c	19	15.4	77.0	1344	22	AAH68297	C glutamicum codin
	20	15.4	77.0	6275	24	ABL32551	Human immune syste
c	21	15.4	77.0	309400	22	AAH68534	C glutamicum codin
c	22	15.2	76.0	1446	21	AAC42071	Arabidopsis thalia
	23	15.2	76.0	2853	23	ABL12631	Drosophila melanog
	24	15.2	76.0	3276	23	ABL02493	Drosophila melanog
	25	15.2	76.0	4505	21	AAA15009	Nucleotide sequenc
c	26	15.2	76.0	5574	23	ABL02492	Drosophila melanog
c	27	15.2	76.0	7243	23	ABL02521	Drosophila melanog
c	28	15.2	76.0	8193	23	ABL12630	Drosophila melanog
c	29	15.2	76.0	21748	23	ABL02520	Drosophila melanog
c	30	15.2	76.0	27426	23	AAS59541	Propionibacterium
	31	15.2	76.0	4403765	22	AAI99683	Mycobacterium tube
	32	15	75.0	27	17	AAT09670	Mycobacterium tube
	33	14.8	74.0	822	23	AAS54258	Pseudomonas aerugi
c	34	14.8	74.0	894	23	AAS51512	Pseudomonas aerugi
	35	14.8	74.0	1167	22	AAF81355	Quorum sensing con
	36	14.8	74.0	2176	15	AAQ57017	PKC nu. Bos tauru
c	37	14.4	72.0	1014	22	AAH65487	C glutamicum codin
c	38	14.4	72.0	1086	23	AAS93170	DNA encoding novel
c	39	14.4	72.0	1086	23	AAS93247	DNA encoding novel
	40	14.4	72.0	1578	21	AAC48875	Arabidopsis thalia
	41	14.4	72.0	1579	21	AAC40928	Arabidopsis thalia
c	42	14.4	72.0	2660	23	ABL10327	Drosophila melanog
	43	14.4	72.0	3342	23	ABL23542	Drosophila melanog
	44	14.4	72.0	3366	23	ABL17225	Drosophila melanog
	45	14.4	72.0	3632	23	ABL13365	Drosophila melanog

ALIGNMENTS

RESULT 1
AAA49824
ID AAA49824 standard; DNA; 20 BP.
XX
AC AAA49824;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene amplification primer rpoB-R.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX

PS Claim 4; Page 4; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene amplification primer rpoB-R (bp
CC 2611-2592). It is used with the forward primer given in AAA49823
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 1 tacggcgtttcgatgaaccc 20

RESULT 2
AAA49826
ID AAA49826 standard; DNA; 20 BP.
XX
AC AAA49826;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-3s.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene sequencing primer rpoB-3s (bp
CC 2611-2592). It is used with the forward primer given in AAA49825 and
CC with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 1 tacggcgtttcgatgaaccc 20

RESULT 3
AAQ61457/c
ID AAQ61457 standard; DNA; 432 BP.
XX
AC AAQ61457;
XX
DT 17-MAY-1994 (first entry)
XX
DE M.tuberculosis rpoB gene fragment.
XX
KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KW mutant; ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9322454-A.
XX
PD 11-NOV-1993.
XX
PF 30-APR-1993; 93WO-EP01063.
XX
PR 17-SEP-1992; 92FR-0011098.
PR 30-APR-1992; 92US-0875940.
PR 14-AUG-1992; 92US-0929206.
PR 16-APR-1993; 93FR-0004545.
XX
PA (ASSI-) ASSISTANCE PUBLIQUE.
PA (INSP) INST PASTEUR.
PA (MEDI-) MEDICAL RES COUNCIL.
PA (UYBE-) UNIV BERNE.
PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
PI Young D, Zhang Y;
XX
DR WPI; 1993-368812/46.
DR P-PSDB; AAR51372.
XX

PT Rapid detection of antibiotic resistance in Mycobacteria - esp.
PT isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in katG, rpoB or rpsL genes
XX
PS Example 2; Fig 13; 97pp; English.
XX
CC PCR amplification was used to obtain rpoB genes from rifampicin-
CC resistant Mycobacterium leprae strains. A comparison with the
CC sequence of the rpoB gene from sensitive strains (AAQ51532) revealed
CC mutations in the region encoding amino acids 400-450. The corresp.
CC region was isolated from M.tuberculosis (AAQ61457). A common
CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
SQ Sequence 432 BP; 78 A; 139 C; 148 G; 67 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 428 TACGGCGTTTCGATGAACCC 409

RESULT 4
AAA49863/c
ID AAA49863 standard; DNA; 480 BP.
XX
AC AAA49863;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene (rifampin resistance).
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; ss.
XX
OS Mycobacterium tuberculosis.
XX
FH Key Location/Qualifiers
FT primer_bind complement(41..60)
FT /*tag= a
FT /note= "primer of AAA49823"
FT primer_bind 372..391
FT /*tag= b
FT /note= "primer of AAA49824"
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Disclosure; Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene (bp2161-2640). Amplification and
CC cycle sequencing primers (see AAA49823-62) are used for the detection
CC and analysis of antibiotic resistance-associated mutations in
CC defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 451 TACGGCGTTTCGATGAACCC 432

RESULT 5
AAT29126/c
ID AAT29126 standard; DNA; 620 BP.
XX
AC AAT29126;
XX
DT 02-DEC-1996 (first entry)
XX
DE rpoB gene fragment (mutant) from Mycobacterium tuberculosis.
XX
KW p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus;
KW Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
KW Staphylococcus; identification; detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US14673.
XX
PR 30-AUG-1995; 95US-0520946.
PR 09-NOV-1994; 94US-0337164.
PR 09-MAR-1995; 95US-0402601.
PR 07-JUN-1995; 95US-0484956.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM;
XX
DR WPI; 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
PS Example 33; Page 306; 433pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene; for
CC identifying strains of microorganisms, especially bacteria selected
CC from the the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the Mycobacterium tuberculosis rpoB gene, which, when
CC mutated is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451Y and S456L mutations. The amplified
CC fragments are given in AAT29124 (Wild type) and AAT29125-26
CC (mutant sequences).
XX
SQ Sequence 620 BP; 103 A; 201 C; 214 G; 102 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
AAT29124/c
ID AAT29124 standard; DNA; 620 BP.
XX
AC AAT29124;
XX
DT 02-DEC-1996 (first entry)
XX
DE rpoB gene fragment from Mycobacterium tuberculosis.
XX
KW p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus;
KW Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
KW Staphylococcus; identification; detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US14673.
XX
PR 30-AUG-1995; 95US-0520946.
PR 09-NOV-1994; 94US-0337164.
PR 09-MAR-1995; 95US-0402601.
PR 07-JUN-1995; 95US-0484956.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM;
XX
DR WPI; 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
PS Example 33; Page 305; 433pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene; for
CC identifying strains of microorganisms, especially bacteria selected
CC from the the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the Mycobacterium tuberculosis rpoB gene, which, when
CC mutated is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451Y and S456L mutations. The amplified
CC fragments are given in AAT29124 (Wild type) and AAT29125-26
CC (mutant sequences).
XX
SQ Sequence 620 BP; 103 A; 202 C; 214 G; 101 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 7
AAT29125/c
ID AAT29125 standard; DNA; 620 BP.
XX
AC AAT29125;
XX
DT 02-DEC-1996 (first entry)
XX
DE rpoB gene fragment (mutant) from Mycobacterium tuberculosis.
XX
KW p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus;
KW Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
KW Staphylococcus; identification; detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US14673.
XX
PR 30-AUG-1995; 95US-0520946.
PR 09-NOV-1994; 94US-0337164.
PR 09-MAR-1995; 95US-0402601.
PR 07-JUN-1995; 95US-0484956.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM;
XX
DR WPI; 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
PS Example 33; Page 305-306; 433pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

```
CC   compared to the cleavage products of reference gene sequences.  The
CC   method is used for detecting mutation in the human p53 gene; for
CC   identifying strains of microorganisms, especially bacteria selected
CC   from the the group of members of the genera Campylobacter,
CC   Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC   The method may also be used for the identification of viruses,
CC   especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC   (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC   region of the Mycobacterium tuberculosis rpoB gene, which, when
CC   mutated is associated with rifampin resistance. The 620 bp region
CC   amplified spans both the H451Y and S456L mutations.  The amplified
CC   fragments are given in AAT29124 (Wild type) and AAT29125-26
CC   (mutant sequences).
XX
SQ   Sequence 620 BP; 103 A; 201 C; 214 G; 102 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 17;  Length 620;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    296 TACGGCGTTTCGATGAACCC 277


RESULT   8
AAT09676/c
ID   AAT09676 standard; DNA; 970 BP.
XX
AC   AAT09676;
XX
DT   15-OCT-1996  (first entry)
XX
DE   Mycobacterium tuberculosis rpoB gene DNA sequence.
XX
KW   Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;
KW   polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.
XX
OS   Mycobacterium tuberculosis.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     10..27
FT                   /*tag=  a
FT                   /note= "primer FENLFF"
FT   primer_bind     226..243
FT                   /*tag=  b
FT                   /note= "primer DDIDHL"
FT   primer_bind     226..240
FT                   /*tag=  c
FT                   /note= "primer DDIDH"
FT   primer_bind     338..364
FT                   /*tag=  d
FT                   /note= "primer rpo95"
FT   primer_bind     348..373
FT                   /*tag=  e
FT                   /note= "primer rpo105"
FT   primer_bind     354..373
FT                   /*tag=  f
FT                   /note= "primer KY290"
FT   misc_feature    372..373
FT                   /*tag=  g
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    433..434
FT                   /*tag=  h
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    438
FT                   /*tag=  i
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    468..469
FT                   /*tag=  j
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    486
FT                   /*tag=  k
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    501
FT                   /*tag=  l
FT                   /note= "M. tuberculosis signature nucleotide"
FT   misc_feature    516
FT                   /*tag=  m
FT                   /note= "M. tuberculosis signature nucleotide"
FT   primer_bind     516..535
FT                   /*tag=  n
FT                   /note= "primer rpo273"
FT   misc_feature    525
FT                   /*tag=  o
FT                   /note= "M. tuberculosis signature nucleotide"
FT   primer_bind     525..541
FT                   /*tag=  p
FT                   /note= "primer KY292"
FT   primer_bind     536..562
FT                   /*tag=  q
FT                   /note= "primer rpo293"
FT   primer_bind     640..666
FT                   /*tag=  r
FT                   /note= "primer rpo397"
FT   primer_bind     952..966
FT                   /*tag=  s
FT                   /note= "primer NMQRQ-1"
FT   primer_bind     952..966
FT                   /*tag=  t
FT                   /note= "primer NMQRQ-2"
XX
PN   WO9533074-A1.
XX
PD   07-DEC-1995.
XX
PF   26-MAY-1995;   95WO-US06790.
XX
PR   26-MAY-1994;   94US-0250030.
XX
PA   (HOFF ) HOFFMANN LA ROCHE INC.
PA   (MAYO-) MAYO FOUNDATION.
XX
PI   Felmlee TA,  Hunt JM,  Persing DH,  Roberts GD,  Whelen AC;
PI   Young KKY;
XX
DR   WPI; 1996-030581/03.
XX
PT   Detection of Mycobacterium tuberculosis - by amplifying sample DNA
PT   with a primer set that targets portions of the gene encoding rpoB.
XX
PS   Disclosure; Fig.3; 54pp; English.
XX
CC   This oligonucleotide DNA primer is specific for Mycobacterium
CC   tuberculosis, and may be used to amplify a sample DNA by targeting
CC   a portion of the gene encoding rpoB.  The 1st several bases comprise a
CC   nonhybridizing tail consisting of filler bases followed by
CC   a restriction site incorporated to facilitate cloning using the
CC   amplicon at a later date, if desired.  The remaining bases hybridize
CC   to bacterial rpoB DNA.  The method provides for the detection of M.
CC   tuberculosis and the concurrent determination of its drug
CC   susceptibility, particularly to rifamycin.  The method can provide
CC   often greater than 95% sensitivity and 100% specificity.  The
CC   biological sample is a fluid or tissue sample from a human.
XX
SQ   Sequence 970 BP; 182 A; 302 C; 330 G; 156 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 17;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 0.39;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    671 TACGGCGTTTCGATGAACCC 652
```

```
RESULT   9
AAH51976/c
ID   AAH51976 standard; DNA; 3519 BP.
XX
AC   AAH51976;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Mycobacterium tuberculosis potential drug target gene SEQ ID 30.
XX
KW   Drug target; growth; organism viability; characterisation; ds.
XX
OS   Mycobacterium tuberculosis.
XX
PN   WO200135317-A1.
XX
PD   17-MAY-2001.
XX
PF   13-NOV-2000; 2000WO-US31152.
XX
PR   12-NOV-1999;   99US-0165086.
PR   12-NOV-1999;   99US-0165124.
PR   01-FEB-2000; 2000US-0179531.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Eisenberg D,  Rotstein SH,  Marcotte EM;
XX
DR   WPI; 2001-329193/34.
DR   P-PSDB; AAG81125.
XX
PT   Identifying nucleotide or polypeptide sequence for use as drug target,
PT   involves providing algorithm that analyzes a functional relationship
PT   between nucleotide or polypeptide sequences, and comparing the
PT   sequences  -
XX
PS   Disclosure; Page 68-69; 207pp; English.
XX
CC   This invention relates to a method for identifying a nucleotide or
CC   polypeptide sequence that may be a drug target, or essential for growth
CC   or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
CC   represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
CC   tuberculosis proteins which are potential drug targets. The DNA and
CC   protein sequences are used to illustrate the method of the invention. The
CC   method involves providing an unknown nucleotide or polypeptide sequences,
CC   and comparing it to a number of sequences along with at least one
CC   algorithm capable of analysing a functional relationship between
CC   nucleotide and polypeptide sequences. The method is useful for
CC   characterising the function of nucleic acids and polypeptides that may be
CC   useful as a target for a drug or essential for the growth or viability of
CC   an organism.
XX
SQ   Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;


  Query Match            100.0%;  Score 20;  DB 22;  Length 3519;
  Best Local Similarity  100.0%;  Pred. No. 0.42;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db   1529 TACGGCGTTTCGATGAACCC 1510


RESULT  10
AAH02079/c
ID   AAH02079 standard; DNA; 3534 BP.
XX
AC   AAH02079;
XX
DT   24-JUL-2001  (first entry)
XX
DE   Mycobacterium tuberculosis nucleotide sequence SEQ ID NO:2072.
XX
KW   Species specific; genus specific; family specific; probe; detection;
KW   identification; algal; archaeal; bacterial; fungal; parasitical;
KW   microorganism; diagnosis; translation elongation factor Tu; toxin;
KW   translation elongation factor G; RecA recombinase; resistance;
KW   catalytic subunit of proton-translocating ATPase; antimicrobial;
KW   vaccine; primer; ds.
XX
OS   Mycobacterium tuberculosis.
XX
PN   WO200123604-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-CA01150.
XX
PR   28-SEP-1999;   99CA-2283458.
PR   19-MAY-2000; 2000CA-2307010.
XX
PA   (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI   Bergeron MG,  Boissinot M,  Huletsky A,  Menard C,  Ouellette M;
PI   Picard FJ,  Roy PH;
XX
DR   WPI; 2001-245006/25.
XX
PT   Nucleic acid sequences are used to generate universal probes and
PT   primers which can be used to identify and detect the presence of algal,
PT   archaeal, bacterial, fungal and parasitical species in a test sample -
XX
PS   Disclosure; Page 1478-1479; 1580pp; English.
XX
CC   The present invention describes a method for generating a repertory of
CC   nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC   and/or primers are derived. The method comprises amplifying the nucleic
CC   acids of determined algal, archaeal, bacterial, fungal and parasitical
CC   species with a combination of defined primer pairs. The method can be
CC   used for producing probes and/or primers for detecting one or more
CC   related microorganisms e.g. algae, archaea, bacteria, fungi and
CC   parasites, for universal detection and for specific and ubiquitous
CC   detection and identification of an algal, archaeal, bacterial, fungal
CC   and parasitical species, genus, family and group. A nucleic acid (I)
CC   obtained using the method of the invention can be used for the universal
CC   detection of any bacterium, fungus or parasite in a sample and for the
CC   detection of at least one antimicrobial agent resistance gene or at
CC   least one toxin gene. hexA nucleic acids are used for the specific and
CC   ubiquitous detection and for identification of Streptococcus pneumoniae.
CC   (I) can be used to design a therapeutic agent which is effective against
CC   microorganisms. Microbial species or genus or family or phylum or group
CC   which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC   Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC   Mycobacteriaceae family, Pseudomonads group, Streptococcus sp.,
CC   Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests
CC   provides faster results than substrate specificity tests as results can
CC   be determined in an hour and improved accuracy is also achieved.
CC   AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
CC   which are given in the exemplification of the present invention.
XX
SQ   Sequence 3534 BP; 679 A; 1081 C; 1188 G; 586 T; 0 other;


  Query Match            100.0%;  Score 20;  DB 22;  Length 3534;
  Best Local Similarity  100.0%;  Pred. No. 0.42;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db   1547 TACGGCGTTTCGATGAACCC 1528


RESULT  11
```

AAA74651/c
ID AAA74651 standard; DNA; 3853 BP.
XX
AC AAA74651;
XX
DT 06-DEC-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene.
XX
KW Mycobacterium tuberculosis; rpoB; RNA polymerase beta subunit;
KW rifampin resistance; mutation detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200043546-A2.
XX
PD 27-JUL-2000.
XX
PF 20-DEC-1999; 99WO-US30377.
XX
PR 19-JAN-1999; 99US-0233996.
XX
PA (DADE-) DADE BEHRING INC.
XX
PI Liu YP, Kurn N;
XX
DR WPI; 2000-524243/47.
XX
PT Method for detecting drug resistance in a strain of an organism,
PT particularly for detecting rifampin resistance in Mycobacterium
PT tuberculosis -
XX
PS Example 1; Fig 4; 86pp; English.
XX
CC The present sequence is the rpoB gene from Mycobacterium tuberculosis.
CC Rifampin resistance is largely associated with point mutations
CC localised in a small core region of 81 base pairs in the rpoB gene, which
CC encodes the RNA polymerase beta subunit. To detect a mutation, a complex
CC is formed comprising a first sequence representing the predetermined
CC region of the gene of the organism and a second sequence representing the
CC corresponding region of the gene of the wild type organism in double
CC stranded form. Each member of at least one pair of non-complementary
CC strands within the complex has a label. The association of the labels in
CC the complex is related to the presence of the mutation. The presence of
CC the mutation is related to the drug resistance of the strain.
XX
SQ Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 2122 TACGGCGTTTCGATGAACCC 2103

RESULT 12
AAA89994/c
ID AAA89994 standard; DNA; 3853 BP.
XX
AC AAA89994;
XX
DT 18-DEC-2000 (first entry)
XX
DE M. tuberculosis rpoB gene encoding RNA polymerase beta subunit.
XX
KW Drug resistance; rifampin; rifampicin; pyrazinamide; rpoB;
KW RNA polymerase beta subunit; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200043545-A2.
XX
PD 27-JUL-2000.
XX
PF 14-DEC-1999; 99WO-US29517.
XX
PR 19-JAN-1999; 99US-0233996.
PR 22-APR-1999; 99US-0296894.
XX
PA (DADE-) DADE BEHRING INC.
XX
PI Liu YP, Kurn N;
XX
DR WPI; 2000-499235/44.
XX
PT Detecting resistance of drugs such as rifampicin in strains of
PT Mycobacterium, comprising detecting mutations in a gene and relating
PT them to drug resistance -
XX
PS Example 1; Fig 4; 91pp; English.
XX
CC This invention relates to a method for detecting drug resistance in a
CC strain of an organism. The method comprises detecting the presence of at
CC least 1 mutation in a first sequence and relating the presence of the
CC mutation to drug resistance. Included in the invention are a kit for
CC carrying out the method and a method for detecting the presence of a
CC difference between two related nucleic acid sequences in an organism. The
CC methods are useful for detecting resistance to drugs such rifampin and
CC pyrazinamide in Mycobacterium. The present sequence represents the
CC Mycobacterium tuberculosis rpoB gene (which encodes the RNA polymerase
CC beta subunit). The sequence is used in an example of the method of the
CC invention for the detection of rifampin resistance in M. tuberculosis.
XX
SQ Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 2122 TACGGCGTTTCGATGAACCC 2103

RESULT 13
AAT12096
ID AAT12096 standard; DNA; 19 BP.
XX
AC AAT12096;
XX
DT 10-JUL-1996 (first entry)
XX
DE M. tuberculosis rpoB gene fragment amplification primer P6.
XX
KW Antibiotic; resistance; spectrum; gene; mycobacterium;
KW determination; amplification; tuberculosis; rpoB; fragment;
KW primer; differential; hybridisation; pattern; rifampicin;
KW rifabutin; species identification; ss.
XX
OS Synthetic.
XX
PN WO9533851-A2.
XX
PD 14-DEC-1995.
XX
PF 09-JUN-1995; 95WO-EP02230.
XX
PR 09-JUN-1994; 94EP-0870093.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI De Beenhouwer H, Jannes G, Machtelinckx L, Portaels F;

PI Rossau R;
XX
DR WPI; 1996-040250/04.
XX
PT Probes and primers for determn. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene
XX
PS Claim 22; Page 39; 69pp; English.
XX
CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT12091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrids formed and
CC inferring the ARS, and opt. the spp., from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampicin and/or rifabutin resistance in M. leprae
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determn.
CC of ARS and spp. identity.
XX
SQ Sequence 19 BP; 4 A; 5 C; 5 G; 5 T; 0 other;

Query Match 95.0%; Score 19; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaacc 19
||||||||||||||||||||
Db 1 tacggcgtttcgatgaacc 19

RESULT 14
AAQ51532/c
ID AAQ51532 standard; DNA; 3447 BP.
XX
AC AAQ51532;
XX
DT 17-MAY-1994 (first entry)
XX
DE M.leprae rpoB gene.
XX
KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KW mutant; ss.
XX
OS Mycobacterium leprae.
XX
FH Key Location/Qualifiers
FT CDS 1..3447
FT /*tag= a
FT /note= "rifampicin-sensitive; in resistant
FT strains the Ser codon (TCG at
FT nucleotides 1273-1275) is often mutated
FT to a Phe, Met or esp. Leu codon"
XX
PN WO9322454-A.
XX
PD 11-NOV-1993.
XX
PF 30-APR-1993; 93WO-EP01063.
XX
PR 17-SEP-1992; 92FR-0011098.
PR 30-APR-1992; 92US-0875940.
PR 14-AUG-1992; 92US-0929206.
PR 16-APR-1993; 93FR-0004545.
XX
PA (ASSI-) ASSISTANCE PUBLIQUE.
PA (INSP) INST PASTEUR.
PA (MEDI-) MEDICAL RES COUNCIL.
PA (UYBE-) UNIV BERNE.
PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
PI Young D, Zhang Y;
XX
DR WPI; 1993-368812/46.
DR P-PSDB; AAR43671.
XX
PT Rapid detection of antibiotic resistance in Mycobacteria - esp.
PT isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in katG, rpoB or rpsL genes
XX
PS Example 2; Fig 12; 97pp; English.
XX
CC PCR amplification was used to obtain rpoB genes from rifampicin-
CC resistant Mycobacterium leprae strains. A comparison with the
CC sequence of the rpoB gene from sensitive strains (AAQ51532) revealed
CC mutations in the region encoding amino acids 400-450. A common
CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
SQ Sequence 3447 BP; 687 A; 965 C; 1139 G; 656 T; 0 other;

Query Match 92.0%; Score 18.4; DB 14; Length 3447;
Best Local Similarity 95.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||| ||||||||||||||
Db 1454 TACGGTGTTTCGATGAACCC 1435

RESULT 15
AAS51357/c
ID AAS51357 standard; DNA; 3474 BP.
XX
AC AAS51357;
XX
DT 13-FEB-2002 (first entry)
XX
DE Enterococcus faecalis DNA for cellular proliferation protein #134.
XX
KW Antisense; ds; prokaryotic cellular proliferation gene;
KW antibiotic; antibacterial; drug design.
XX
OS Enterococcus faecalis.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR P-PSDB; AAU33498.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
PS Claim 27; Seq ID No 3939; 511pp; English.

XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence encodes an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 3474 BP; 1074 A; 691 C; 776 G; 933 T; 0 other;

Query Match 84.0%; Score 16.8; DB 23; Length 3474;
Best Local Similarity 90.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
|| |||||||||||||| ||
Db 1652 TAAGGCGTTTCGATGAAACC 1633

Search completed: August 7, 2002, 22:04:01
Job time: 8061 sec

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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:51:37 ; Search time 2167.9 Seconds
(without alignments)
193.058 Million cell updates/sec

Title: US-09-786-105-2
Perfect score: 20
Sequence: 1 tacggcgtttcgatgaaccc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	20	100.0	432	1	MSGRIFRNAP	L05910 Mycobacteri
c 2	20	100.0	432	6	AR067448	AR067448 Sequence
c 3	20	100.0	620	6	AR062056	AR062056 Sequence
c 4	20	100.0	620	6	AR062057	AR062057 Sequence
c 5	20	100.0	620	6	AR062058	AR062058 Sequence
6	20	100.0	620	6	AR062059	AR062059 Sequence
7	20	100.0	620	6	AR062060	AR062060 Sequence
8	20	100.0	620	6	AR062061	AR062061 Sequence
c 9	20	100.0	705	1	AF060353	AF060353 Mycobacte
c 10	20	100.0	706	6	AR149128	AR149128 Sequence
c 11	20	100.0	970	6	I50706	I50706 Sequence 1
c 12	20	100.0	3534	6	AX111339	AX111339 Sequence
c 13	20	100.0	3853	1	MTU12205	U12205 Mycobacteri
c 14	20	100.0	5084	1	MSGRPOB	L27989 Mycobacteri
c 15	20	100.0	19352	1	AE006964	AE006964 Mycobacte
c 16	20	100.0	19770	1	MTCI376	Z95972 Mycobacteri
c 17	18.4	92.0	626	1	AF060295	AF060295 Mycobacte
c 18	18.4	92.0	703	1	AF060349	AF060349 Mycobacte
c 19	18.4	92.0	705	1	AF060279	AF060279 Mycobacte
c 20	18.4	92.0	705	1	AF060290	AF060290 Mycobacte
c 21	18.4	92.0	705	1	AF060293	AF060293 Mycobacte
c 22	18.4	92.0	705	1	AF060297	AF060297 Mycobacte
c 23	18.4	92.0	705	1	AF060299	AF060299 Mycobacte
c 24	18.4	92.0	705	1	AF060300	AF060300 Mycobacte
c 25	18.4	92.0	705	1	AF060325	AF060325 Mycobacte
c 26	18.4	92.0	705	1	AF060326	AF060326 Mycobacte
c 27	18.4	92.0	705	1	AF060327	AF060327 Mycobacte
c 28	18.4	92.0	705	1	AF060328	AF060328 Mycobacte
c 29	18.4	92.0	705	1	AF060329	AF060329 Mycobacte
c 30	18.4	92.0	705	1	AF060331	AF060331 Mycobacte
c 31	18.4	92.0	705	1	AF060351	AF060351 Mycobacte
c 32	18.4	92.0	705	1	AF060366	AF060366 Mycobacte
c 33	18.4	92.0	3316	1	AF172323	AF172323 Bacillus
c 34	18.4	92.0	3447	6	AR067447	AR067447 Sequence
c 35	18.4	92.0	37617	1	MLB1790G	Z14314 M.leprae ge
36	18.4	92.0	348950	1	MLEPRTN7	AL583923 Mycobacte
c 37	17.4	87.0	10909	1	AE007977	AE007977 Agrobacte
c 38	17.4	87.0	13047	1	AE009010	AE009010 Agrobacte
39	16.8	84.0	518	1	AF325874	AF325874 Staphyloc
c 40	16.8	84.0	643	1	AF060346	AF060346 Mycobacte
c 41	16.8	84.0	647	1	AF060350	AF060350 Mycobacte
c 42	16.8	84.0	652	1	AF060344	AF060344 Mycobacte
c 43	16.8	84.0	652	1	AF060364	AF060364 Mycobacte
c 44	16.8	84.0	705	1	AF060283	AF060283 Mycobacte
c 45	16.8	84.0	705	1	AF060285	AF060285 Mycobacte

ALIGNMENTS

RESULT 1
MSGRIFRNAP/c
LOCUS MSGRIFRNAP 432 bp DNA linear BCT 21-MAY-1993
DEFINITION Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin resistance gene, complete cds.
ACCESSION L05910
VERSION L05910.1 GI:149991
KEYWORDS RNA polymerase beta-subunit; rifampicin resistance.
SOURCE Mycobacterium tuberculosis (strain H37) DNA.
ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 432)
AUTHORS Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T.,
Colston,J., Matter,L., Schopfer,K. and Bodmer,T.
TITLE Detection of rifampicin-resistance mutation in Mycobacterium tuberculosis
JOURNAL Antimicrob. Agents Chemother. 341, 647-650 (1993)
FEATURES Location/Qualifiers
source 1. .432
/organism="Mycobacterium tuberculosis"
/strain="H37"

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                /db_xref="GI:149992"
                /translation="GNRRLRTVGELIQNQIRVGMSRMERVVRERMTTQDVEAITPQTL
                INIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDV
                HPSHYGRMCPIETPEGPNIGLIGSLSVYARVNPFGFIETPYR"
     variation  149
                /phenotype="rifampicin resistant in association with
                mutation 234 G"
                /replace="c"
     variation  188
                /phenotype="rifampicin resistant"
                /replace="c"
     variation  191
                /phenotype="rifampicin resistant in association with
                mutation 203 T"
                /replace="c"
     variation  194
                /phenotype="rifampicin resistant"
                /replace="t"
     variation  203
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                /replace="t"
     variation  208. .210
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                /replace=""
     variation  232
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     variation  232
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                /replace="a"
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     variation  233
                /phenotype="rifampicin resistant"
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     variation  234
                /phenotype="rifampicin resistant"
                /replace="g"
     variation  247. .248
                /phenotype="rifampicin resistant"
                /replace="ca"
     variation  248
                /phenotype="rifampicin resistant"
                /replace="g"
     variation  248
                /phenotype="rifampicin resistant"
                /replace="t"
     variation  254
                /phenotype="rifampicin resistant"
                /replace="c"
BASE COUNT       77 a    140 c    148 g     67 t
ORIGIN


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  Best Local Similarity  100.0%;  Pred. No. 1.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
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Db    428 TACGGCGTTTCGATGAACCC 409


RESULT   2
AR067448/c
LOCUS       AR067448               432 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 59 from patent US 5851763.
ACCESSION   AR067448
VERSION     AR067448.1  GI:5998670
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 432)
  AUTHORS   Heym,B., Cole,S., Young,D., Zhang,Y., Honore,N., Telenti,A. and
            Bodmer,T.
  TITLE     Rapid detection of antibiotic resistance in mycobacterium
            tuberculosis
  JOURNAL   Patent: US 5851763-A 59 22-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .432
                     /organism="unknown"
BASE COUNT       77 a    139 c    149 g     67 t
ORIGIN


  Query Match           100.0%;  Score 20;  DB 6;  Length 432;
  Best Local Similarity  100.0%;  Pred. No. 1.3;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    428 TACGGCGTTTCGATGAACCC 409


RESULT   3
AR062056/c
LOCUS       AR062056               620 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 135 from patent US 5843669.
ACCESSION   AR062056
VERSION     AR062056.1  GI:5989747
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
  TITLE     Cleavage of nucleic acid acid using thermostable methoanococcus
            jannaschii FEN-1 endonucleases
  JOURNAL   Patent: US 5843669-A 135 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .620
                     /organism="unknown"
BASE COUNT      103 a    202 c    214 g    101 t
ORIGIN


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  Best Local Similarity  100.0%;  Pred. No. 1.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    296 TACGGCGTTTCGATGAACCC 277


RESULT   4
AR062057/c
LOCUS       AR062057               620 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 136 from patent US 5843669.
ACCESSION   AR062057
VERSION     AR062057.1  GI:5989748
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
  TITLE     Cleavage of nucleic acid acid using thermostable methoanococcus
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jannaschii FEN-1 endonucleases
JOURNAL Patent: US 5843669-A 136 01-DEC-1998;
FEATURES Location/Qualifiers
source 1. .620
/organism="unknown"
BASE COUNT 103 a 201 c 214 g 102 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 5
AR062058/c
LOCUS AR062058 620 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 137 from patent US 5843669.
ACCESSION AR062058
VERSION AR062058.1 GI:5989749
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methoanococcus
jannaschii FEN-1 endonucleases
JOURNAL Patent: US 5843669-A 137 01-DEC-1998;
FEATURES Location/Qualifiers
source 1. .620
/organism="unknown"
BASE COUNT 103 a 201 c 214 g 102 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
AR062059
LOCUS AR062059 620 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 138 from patent US 5843669.
ACCESSION AR062059
VERSION AR062059.1 GI:5989750
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methoanococcus
jannaschii FEN-1 endonucleases
JOURNAL Patent: US 5843669-A 138 01-DEC-1998;
FEATURES Location/Qualifiers
source 1. .620
/organism="unknown"
BASE COUNT 101 a 214 c 202 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 7
AR062060
LOCUS AR062060 620 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 139 from patent US 5843669.
ACCESSION AR062060
VERSION AR062060.1 GI:5989751
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methoanococcus
jannaschii FEN-1 endonucleases
JOURNAL Patent: US 5843669-A 139 01-DEC-1998;
FEATURES Location/Qualifiers
source 1. .620
/organism="unknown"
BASE COUNT 102 a 214 c 201 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 8
AR062061
LOCUS AR062061 620 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 140 from patent US 5843669.
ACCESSION AR062061
VERSION AR062061.1 GI:5989752
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methoanococcus
jannaschii FEN-1 endonucleases
JOURNAL Patent: US 5843669-A 140 01-DEC-1998;
FEATURES Location/Qualifiers
source 1. .620
/organism="unknown"
BASE COUNT 102 a 214 c 201 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgtttcgatgaaccc 20
||||||||||||||||||||
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 9
AF060353/c
LOCUS AF060353 705 bp DNA linear BCT 15-MAY-1998
DEFINITION Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB) gene,

```
            partial cds.
ACCESSION   AF060353
VERSION     AF060353.1  GI:3133464
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 705)
  AUTHORS   Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
            Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
  TITLE     Simultaneous genotyping and species identification using
            hybridization pattern recognition analysis of generic mycobacterium
            DNA arrays
  JOURNAL   Genome Res. 8 (5), 435-448 (1998)
  MEDLINE   98248685
REFERENCE   2  (bases 1 to 705)
  AUTHORS   Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
            Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-APR-1998) Division of Infectious Disease, Affymetrix,
            3380 Central Expressway, Santa Clara, CA 95051, USA
FEATURES             Location/Qualifiers
     source          1. .705
                     /organism="Mycobacterium tuberculosis"
                     /strain="ATCC27294"
                     /db_xref="ATCC:27294"
                     /db_xref="taxon:1773"
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                     /gene="rpoB"
     CDS             <1. .>705
                     /gene="rpoB"
                     /codon_start=3
                     /transl_table=11
                     /product="RNA polymerase beta-subunit"
                     /protein_id="AAC38533.1"
                     /db_xref="GI:3133465"
                     /translation="QDVEAITPQTLINIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLT
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                     FGFIETPYRKVVDGVVSDEIVYLTADEEDRHVVAQANSPIDADGRFVEPRVLVRRKAG
                     EVEYVPSSEVDYMDVSPRQMVSVATAMIPFLEHDDANRALMGANMQRQAVPLVRSEAP
                     LVGTGMELRAAIDAAT"
BASE COUNT      117 a    227 c    250 g    111 t
ORIGIN
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  Query Match             100.0%;  Score 20;  DB 1;  Length 705;
  Best Local Similarity   100.0%;  Pred. No. 1.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    331 TACGGCGTTTCGATGAACCC 312
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RESULT  10
AR149128/c
LOCUS       AR149128                706 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 24 from patent US 6228575.
ACCESSION   AR149128
VERSION     AR149128.1  GI:15113719
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 706)
  AUTHORS   Gingeras,T.R., Mack,D., Chee,M.S., Berno,A.J., Stryer,L.,
            Ghandour,G. and Wang,C.
  TITLE     Chip-based species identification and phenotypic characterization
            of microorganisms
  JOURNAL   Patent: US 6228575-A 24 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .706
                     /organism="unknown"
BASE COUNT      117 a    227 c    250 g    111 t      1 others
ORIGIN
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  Query Match             100.0%;  Score 20;  DB 6;  Length 706;
  Best Local Similarity   100.0%;  Pred. No. 1.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    332 TACGGCGTTTCGATGAACCC 313
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RESULT  11
I50706/c
LOCUS       I50706                  970 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1 from patent US 5643723.
ACCESSION   I50706
VERSION     I50706.1  GI:2472409
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 970)
  AUTHORS   Persing,D.H., Hunt,J.J., Young,K.K.Y., Felmlee,T.A., Roberts,G.D.
            and Whelan,A.Christian.
  TITLE     Detection of a genetic locus encoding resistance to rifampin in
            mycobacterial cultures and in clinical specimens
  JOURNAL   Patent: US 5643723-A 1 01-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .970
                     /organism="unknown"
BASE COUNT      182 a    302 c    330 g    156 t
ORIGIN
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  Query Match             100.0%;  Score 20;  DB 6;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db    671 TACGGCGTTTCGATGAACCC 652
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RESULT  12
AX111339/c
LOCUS       AX111339                3534 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 2072 from Patent WO0123604.
ACCESSION   AX111339
VERSION     AX111339.1  GI:13927631
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 3534)
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 2072 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .3534
                     /organism="Mycobacterium tuberculosis"
                     /strain="Rv"
                     /db_xref="taxon:1773"
BASE COUNT      679 a   1081 c   1188 g    586 t
ORIGIN
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  Query Match           100.0%;  Score 20;  DB 6;  Length 3534;
  Best Local Similarity  100.0%;  Pred. No. 1.9;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
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Db   1547 TACGGCGTTTCGATGAACCC 1528


RESULT 13
MTU12205/c
LOCUS       MTU12205                3853 bp    DNA     linear   BCT 02-MAR-2000
DEFINITION  Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
            gene, partial cds.
ACCESSION   U12205
VERSION     U12205.1  GI:515684
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 3853)
  AUTHORS   Imboden,P., Troller,R., Marchesi,F., Telenti,A., Bodmer,T.,
            Cole,S., Schopfer,K. and Burkart,T.
  TITLE     The rpoB gene of Mycobacterium tuberculosis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3853)
  AUTHORS   Imboden,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-1994) Paul Imboden, Institute for Medical
            Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
            3010, Switzerland
FEATURES             Location/Qualifiers
     source          1. .3853
                     /organism="Mycobacterium tuberculosis"
                     /strain="H37Rv"
                     /db_xref="taxon:1773"
     gene            576. .>3853
                     /gene="rpoB"
     CDS             576. .>3853
                     /gene="rpoB"
                     /codon_start=1
                     /transl_table=11
                     /product="RNA-polymerase beta subunit"
                     /protein_id="AAA20242.2"
                     /db_xref="GI:7144499"
                     /translation="MLEGCILADSRQSKTAASPSPSRPQSSSNNSVPGAPNRVSFAKL
                     REPLEVPGLLDVQTDSFEWLIGSPRWRESAAERGDVNPVGGLEEVLYELSPIEDFSGS
                     MSLSFSDPRFDDVKAPVDECKDKDMTYAAPLFVTAEFINNNTGEIKSQTVFMGDFPMM
                     TEKGTFIINGTERVVVSQLVRSPGVYFDETIDKSTDKTLHSVKVIPSRGAWLEFDVDK
                     RDTVGVRIDRKRRQPVTVLLKALGWTSEQIVERFGFSEIMRSTLEKDNTVGTDEALLD
                     IYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARVGRYKVNKKLGLHVGEPITSSTLT
                     EEDVVATIEYLVRLHEGQTTMTVPGGVEVPVETDDIDHFGNRRLRTVGELIQNQIRVG
                     MSRMERVVRERMTTQDVEAITPQTLINIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLT
                     HKRRLSALGPGGLSRERAGLEVRDVHPSHYGRMCPIETPEGPNIGLIGSLSVYARVNP
                     FGFIETPYRKVVDGVVSDGIVYLTADEEDRHVVAQANSPIDADGRFVEPRVLVRRKAG
                     EVEYVPSSEVDYMDVSPRQMVSVATAMIPFLEHDDANRALMGANMQRQAVPLVRSEAP
                     LVGTGMELRAAIDAATSSSQESGVIEEVSADYITVMHDNGTRRTYRMRKFARSNHGTC
                     ANQCPIVDAGDRVEAGQVIADGPCTDDGEMALGKNLLVAIMPWEGHNYEDAIILSNRL
                     VEEDVLTSIHIEEHEIDARDTKLGAEEITRDIPNISDEVLADLDERGIVRIGAEVRDG
                     DILVGKVTPKGETELTPEERLLRAIFGEKAREVRDTSLKVPHGESGKVIGIRVFSRED
                     EDELPAGVNELVRVYVAQKRKISDGDKLAGRHGNKGVIGKILPVEDMPFLADGTPVDI
                     ILNTHGVPRRMNIGQILETHLGWCAHSGWKVDAAKGVPDWAARLPDELLEAQPNAIVS
                     TPVFDGAQEAELQGLLSCTLPNRDGDVLVDADGKAMLFDGRSGEPFPYPVTVGYMYIM
                     KLHHLVDDKIHARSTGPYSMITQQPLGGKAQFGGQRFGEMECWAMQAYGAAYTLQELL
                     TIKS"
BASE COUNT      723 a   1173 c   1293 g    664 t
ORIGIN
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  Query Match           100.0%;  Score 20;  DB 1;  Length 3853;
  Best Local Similarity  100.0%;  Pred. No. 2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
          ||||||||||||||||||||
Db   2122 TACGGCGTTTCGATGAACCC 2103


RESULT 14
MSGRPOB/c
LOCUS       MSGRPOB                 5084 bp    DNA     linear   BCT 13-SEP-1994
DEFINITION  Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB)
            gene, complete cds and RNA polymerase beta'-subunit rpoC gene,
            partial cds.
ACCESSION   L27989
VERSION     L27989.1  GI:468333
KEYWORDS    RNA polymerase beta-subunit; rpoB gene.
SOURCE      Mycobacterium tuberculosis (strain Rv) DNA.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 5084)
  AUTHORS   Miller,L.P., Crawford,J.T. and Shinnick,T.M.
  TITLE     The rpoB gene of Mycobacterium tuberculosis
  JOURNAL   Antimicrob. Agents Chemother. 38 (4), 805-811 (1994)
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Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
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DEFINITION Mycobacterium tuberculosis CDC1551, section 50 of 280 of the complete genome.
ACCESSION AE006964 AE000516
VERSION AE006964.1 GI:13880217
KEYWORDS .
SOURCE Mycobacterium tuberculosis CDC1551.
ORGANISM Mycobacterium tuberculosis CDC1551
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 19352)
AUTHORS Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O., Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E., Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M., Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H., Gill,J., Mikula,A. and Bishai,W.
TITLE Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 19352)
AUTHORS Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O., Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E., Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M., Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H., Gill,J., Mikula,A. and Bishai,W.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
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GenCore version 4.5

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	20	100.0	306	4	US-09-147-935A-50	Sequence 50, Appl
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8	20	100.0	432	3	US-09-082-614A-59	Sequence 59, Appl
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ALIGNMENTS

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; Patent No. 6329138
;  GENERAL INFORMATION:
;    APPLICANT:  DE BEENHOUWER, HANS
;    APPLICANT:  PORTAELS, FRAN OISE
;    APPLICANT:  MACHTELINCKX, LIEVE
;    APPLICANT:  JANNES, GEERT
;    APPLICANT:  ROSSAU, RUDI
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF THE ANTIBIOTIC
;    TITLE OF INVENTION:  RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  US
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/750,088A
;      FILING DATE:  21-FEB-1997
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GOLDSTEIN, JORGE A.
;      REGISTRATION NUMBER:  29,021
;      REFERENCE/DOCKET NUMBER:  1657.0010000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  70:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-750-088A-70


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; Sequence 2, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 2
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium africanum
US-09-147-935A-2


  Query Match             100.0%;  Score 20;  DB 4;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 tacggtcggcgagctgatcc 24


RESULT   3
US-09-147-935A-6
; Sequence 6, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 6
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium bovis
US-09-147-935A-6


  Query Match             100.0%;  Score 20;  DB 4;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 tacggtcggcgagctgatcc 24


RESULT   4
US-09-147-935A-7
; Sequence 7, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 7
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium bovis BCG
US-09-147-935A-7


  Query Match             100.0%;  Score 20;  DB 4;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 tacggtcggcgagctgatcc 24


RESULT   5
US-09-147-935A-41
; Sequence 41, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:     KOPATIN 1.0
; SEQ ID NO 41
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-41


  Query Match             100.0%;  Score 20;  DB 4;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 tacggtcggcgagctgatcc 24


RESULT   6
US-09-147-935A-50
; Sequence 50, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:   A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
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;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:     50
;  SOFTWARE:      KOPATIN 1.0
; SEQ ID NO 50
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-50


  Query Match            100.0%;  Score 20;  DB 4;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 0.24;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 tacggtcggcgagctgatcc 24


RESULT   7
US-08-313-185-59
; Sequence 59, Application US/08313185
; Patent No. 5851763
;  GENERAL INFORMATION:
;    APPLICANT:  Heym, Beate
;    APPLICANT:  Cole, Stewart
;    APPLICANT:  Young, Douglas
;    APPLICANT:  Zhang, Ying
;    APPLICANT:  Honore, Nadine
;    APPLICANT:  Telenti, Amalio
;    APPLICANT:  Bodmer, Thomas
;    TITLE OF INVENTION:  Rapid Detection of Antibiotic Resistance
;    TITLE OF INVENTION:  in Mycobacterium Tuberculosis
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/313,185
;      FILING DATE:  12-OCT-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  02356.0068-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-313-185-59


  Query Match            100.0%;  Score 20;  DB 2;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 0.25;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db     18 TACGGTCGGCGAGCTGATCC 37


RESULT   8
US-09-082-614A-59
; Sequence 59, Application US/09082614A
; Patent No. 6124098
;  GENERAL INFORMATION:
;    APPLICANT:  Heym, Beate
;    APPLICANT:  Cole, Stewart
;    APPLICANT:  Young, Douglas
;    APPLICANT:  Zhang, Ying
;    APPLICANT:  Honore, Nadine
;    APPLICANT:  Telenti, Amalio
;    APPLICANT:  Bodmer, Thomas
;    TITLE OF INVENTION:  Rapid Detection of Antibiotic Resistance
;    TITLE OF INVENTION:  in Mycobacterium Tuberculosis
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/082,614A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/313,185
;      FILING DATE:  12-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  02356.0068-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-082-614A-59


  Query Match            100.0%;  Score 20;  DB 3;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 0.25;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db     18 TACGGTCGGCGAGCTGATCC 37


RESULT   9
US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
;  GENERAL INFORMATION:
;    APPLICANT:  Persing, David H.
;    TITLE OF INVENTION:  Detection of a Genetic Locus Encoding
;    TITLE OF INVENTION:  Resistance to Rifampin in Mycobacterial Cultures and in
```

```
;    TITLE OF INVENTION:  Clinical Specimens
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schwegman, Lundberg & Woessner
;      STREET:  3500 IDS Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/250,030
;      FILING DATE:  26-MAY-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mueting, Ann M.
;      REGISTRATION NUMBER:  33,977
;      REFERENCE/DOCKET NUMBER:  150.105US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-339-0331
;      TELEFAX:  612-339-3061
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  970 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-250-030-1


  Query Match             100.0%;  Score 20;  DB 1;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 0.25;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db    261 TACGGTCGGCGAGCTGATCC 280


RESULT  10
PCT-US95-06790-1
; Sequence 1, Application PC/TUS9506790
;  GENERAL INFORMATION:
;    APPLICANT:  Mayo Foundation for Medical Education and Research
;    APPLICANT:  and Hoffmann-La Roche Inc.
;    TITLE OF INVENTION:  Detection of a Genetic Locus Encoding
;    TITLE OF INVENTION:  Resistance to Rifampin
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schwegman, Lundberg & Woessner
;      STREET:  3500 IDS Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/06790
;      FILING DATE:  26-MAY-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Raasch, Kevin W.
;      REGISTRATION NUMBER:  35,651
;      REFERENCE/DOCKET NUMBER:  150.105WO1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-339-0331
;      TELEFAX:  612-339-3061
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  970 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
PCT-US95-06790-1


  Query Match             100.0%;  Score 20;  DB 5;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 0.25;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db    261 TACGGTCGGCGAGCTGATCC 280


RESULT  11
US-09-147-935A-44
; Sequence 44, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:  A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:  50
;  SOFTWARE:  KOPATIN 1.0
; SEQ ID NO 44
;  LENGTH: 306
;  TYPE: DNA
;  ORGANISM: Mycobacterium xenopi
US-09-147-935A-44


  Query Match             95.0%;  Score 19;  DB 4;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 0.75;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 acggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      6 acggtcggcgagctgatcc 24


RESULT  12
US-08-750-088A-30
; Sequence 30, Application US/08750088A
; Patent No. 6329138
;  GENERAL INFORMATION:
;    APPLICANT:  DE BEENHOUWER, HANS
;    APPLICANT:  PORTAELS, FRAN OISE
;    APPLICANT:  MACHTELINCKX, LIEVE
;    APPLICANT:  JANNES, GEERT
;    APPLICANT:  ROSSAU, RUDI
;    TITLE OF INVENTION:  METHOD FOR DETECTION OF THE ANTIBIOTIC
;    TITLE OF INVENTION:  RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  US
```

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;       ZIP:  20005-3934
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/750,088A
;       FILING DATE:  21-FEB-1997
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  GOLDSTEIN, JORGE A.
;       REGISTRATION NUMBER:  29,021
;       REFERENCE/DOCKET NUMBER:  1657.0010000
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2540
;   INFORMATION FOR SEQ ID NO:  30:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  25 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-750-088A-30


  Query Match             92.0%;  Score 18.4;  DB 4;  Length 25;
  Best Local Similarity   95.0%;  Pred. No. 1.4;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          | ||||||||||||||||||
Db      6 TTCGGTCGGCGAGCTGATCC 25


RESULT  13
US-09-147-935A-4
; Sequence 4, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:  A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:  50
;  SOFTWARE:  KOPATIN 1.0
; SEQ ID NO 4
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium aurum
US-09-147-935A-4


  Query Match             92.0%;  Score 18.4;  DB 4;  Length 306;
  Best Local Similarity   95.0%;  Pred. No. 1.5;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||| ||||||||||||||||
Db      5 taccgtcggcgagctgatcc 24


RESULT  14
US-09-147-935A-9
; Sequence 9, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:  A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:  50
;  SOFTWARE:  KOPATIN 1.0
; SEQ ID NO 9
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium celatum Type2
US-09-147-935A-9


  Query Match             92.0%;  Score 18.4;  DB 4;  Length 306;
  Best Local Similarity   95.0%;  Pred. No. 1.5;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||| ||||||||||||||||
Db      5 taccgtcggcgagctgatcc 24


RESULT  15
US-09-147-935A-10
; Sequence 10, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
;  APPLICANT:  KOOK, Yoon-Hoh
;  APPLICANT:  KIM, Bum-Joon
;  TITLE OF INVENTION:  A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;  FILE REFERENCE:  0136/0F425
;  CURRENT APPLICATION NUMBER: US/09/147,935A
;  CURRENT FILING DATE:  1999-03-19
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
;  PRIOR FILING DATE:  1998-07-28
;  NUMBER OF SEQ ID NOS:  50
;  SOFTWARE:  KOPATIN 1.0
; SEQ ID NO 10
;   LENGTH: 306
;   TYPE: DNA
;   ORGANISM: Mycobacterium chelonae
US-09-147-935A-10


  Query Match             92.0%;  Score 18.4;  DB 4;  Length 306;
  Best Local Similarity   95.0%;  Pred. No. 1.5;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||| ||||||||||||||||
Db      5 taccgtcggcgagctgatcc 24


Search completed: August  7, 2002, 21:54:16
Job time: 24011 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 14:53:50 ; Search time 4103.44 Seconds
(without alignments)
65.784 Million cell updates/sec

Title: US-09-786-105-1
Perfect score: 20
Sequence: 1 tacggtcggcgagctgatcc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	18.4	92.0	130	10	BM397871	BM397871 5009-0-38
c	2	18.4	92.0	132	10	BM396091	BM396091 5009-0-17
c	3	18.4	92.0	134	10	BM398255	BM398255 5009-0-42
c	4	17.4	87.0	984	12	CNS01GJZ	AL143232 Anopheles
	5	17	85.0	422	10	BE443802	BE443802 WHE1122_B
	6	17	85.0	544	10	BE445100	BE445100 WHE1132_H
	7	17	85.0	558	10	BE444713	BE444713 WHE1137_H
	8	17	85.0	610	9	BE195103	BE195103 HVSMEh008
	9	17	85.0	658	10	BE442518	BE442518 WHE1101_H
	10	17	85.0	828	10	BG299722	BG299722 HVSMEa002
c	11	16.8	84.0	419	10	BI188703	BI188703 d2e05fs.r
c	12	16.8	84.0	606	10	BI981973	BI981973 fu53f08.y
c	13	16.8	84.0	640	10	BI888442	BI888442 ZF637-2-0
	14	16.4	82.0	292	9	AW502654	AW502654 UI-HF-BR0
	15	16.4	82.0	338	9	AW501791	AW501791 UI-HF-BR0
c	16	16.4	82.0	402	9	BE101908	BE101908 UI-R-BO1-
	17	16.4	82.0	460	9	AW502300	AW502300 UI-HF-BR0
	18	16.4	82.0	470	9	AW502130	AW502130 UI-HF-BR0
	19	16.4	82.0	586	10	BM321268	BM321268 rockefell
	20	16.4	82.0	653	10	BM320964	BM320964 rockefell
	21	16.4	82.0	712	10	BM321334	BM321334 rockefell
	22	16.4	82.0	899	10	BM320891	BM320891 rockefell
	23	16	80.0	708	10	BE585978	BE585978 Est#7pT7_
	24	15.8	79.0	197	6	BE599873	Be599873 PI1_80_G0
	25	15.8	79.0	197	10	BM318366	BM318366 PI1_77_G0
c	26	15.8	79.0	315	10	BE419003	BE419003 WWR020.D1
	27	15.8	79.0	360	10	BG412215	BG412215 OV2_39_C0
c	28	15.8	79.0	411	10	BG263401	BG263401 WHE2341_E
c	29	15.8	79.0	428	9	AI967080	AI967080 496021E08
c	30	15.8	79.0	451	10	C72862	C72862 C72862 Rice
c	31	15.8	79.0	461	10	C28055	C28055 C28055 Rice
c	32	15.8	79.0	493	9	BE215753	BE215753 HV_CEb000
	33	15.8	79.0	507	6	BE599649	Be599649 PI1_78_A0
	34	15.8	79.0	507	10	BM318224	BM318224 PI1_79_A0
	35	15.8	79.0	560	10	BG411877	BG411877 OV2_39_C0
	36	15.8	79.0	565	12	AZ178000	AZ178000 SP_0149_A
c	37	15.8	79.0	597	12	BH402082	BH402082 AG-ND-156
	38	15.8	79.0	605	9	AL508804	AL508804 AL508804
c	39	15.8	79.0	672	9	BB316372	BB316372 BB316372
c	40	15.8	79.0	726	12	AZ359615	AZ359615 1M0102G02
	41	15.8	79.0	740	12	BH016284	BH016284 TDGCK39TH
	42	15.8	79.0	841	10	BI544719	BI544719 603242678
c	43	15.8	79.0	880	10	BI911230	BI911230 603062995
	44	15.8	79.0	946	10	BG475629	BG475629 602520553
c	45	15.8	79.0	1077	12	CNS07739	AL432187 T3 end of

ALIGNMENTS

RESULT 1
BM397871/c
LOCUS BM397871 130 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-38-C10.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM397871
VERSION BM397871.1 GI:18197924
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 130)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel ,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .130
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT 26 a 41 c 44 g 18 t 1 others
ORIGIN

Query Match 92.0%; Score 18.4; DB 10; Length 130;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;

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  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||| ||||||||||||||||
Db     94 TACCGTCGGCGAGCTGATCC 75


RESULT   2
BM396091/c
LOCUS       BM396091                 132 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-17-B01.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM396091
VERSION     BM396091.1  GI:18196144
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila.
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1  (bases 1 to 132)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
            ,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .132
                     /organism="Tetrahymena thermophila"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT       27 a     42 c     44 g     19 t
ORIGIN


  Query Match             92.0%;  Score 18.4;  DB 10;  Length 132;
  Best Local Similarity   95.0%;  Pred. No. 1.7e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||| ||||||||||||||||
Db     96 TACCGTCGGCGAGCTGATCC 77


RESULT   3
BM398255/c
LOCUS       BM398255                 134 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-42-H08.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM398255
VERSION     BM398255.1  GI:18198308
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila.
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1  (bases 1 to 134)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
            ,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .134
                     /organism="Tetrahymena thermophila"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT       26 a     44 c     46 g     18 t
ORIGIN


  Query Match             92.0%;  Score 18.4;  DB 10;  Length 134;
  Best Local Similarity   95.0%;  Pred. No. 1.7e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||| ||||||||||||||||
Db     98 TACCGTCGGCGAGCTGATCC 79


RESULT   4
CNS01GJZ/c
LOCUS       CNS01GJZ                 984 bp    DNA     linear   GSS 01-JUN-2001
DEFINITION  Anopheles gambiae GSS T7 end of clone 06016 of NotreDame1 library
            from strain PEST of Anopheles gambiae (African malaria mosquito),
            genomic survey sequence.
ACCESSION   AL143232
VERSION     AL143232.1  GI:7001389
KEYWORDS    GSS.
SOURCE      African malaria mosquito.
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
            Culicoidea; Anopheles.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
REFERENCE   2  (bases 1 to 984)
  AUTHORS   Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
            Roux, Paris 75015, France
COMMENT     This clone is from an A. gambiae BAC library provided by F.H.
            Collins and sequenced by Genoscope in collaboration with the
            Laboratory of Biochem. and Biol. Molec. of Insects, Institut
            Pasteur.
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="Anopheles gambiae"
                     /strain="PEST"
                     /db_xref="taxon:7165"
                     /clone="06016"
                     /clone_lib="NotreDame1"
                     /note="end : T7"
BASE COUNT      272 a    236 c    241 g    232 t      3 others
ORIGIN


  Query Match             87.0%;  Score 17.4;  DB 12;  Length 984;
  Best Local Similarity   94.7%;  Pred. No. 7.4e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy      1 tacggtcggcgagctgatc 19
          ||||||||||||||| |||
Db    103 TACGGTCGGCGAGCTAATC 85


RESULT   5
BE443802
LOCUS       BE443802                422 bp    mRNA    linear   EST 25-JUL-2000
DEFINITION  WHE1122_B06_C12ZS Wheat etiolated seedling root normalized cDNA
            library Triticum aestivum cDNA clone WHE1122_B06_C12, mRNA
            sequence.
ACCESSION   BE443802
VERSION     BE443802.1  GI:9443341
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 422)
  AUTHORS   Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
            ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
            Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Normalized root cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES             Location/Qualifiers
     source          1. .422
                     /organism="Triticum aestivum"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="WHE1122_B06_C12"
                     /clone_lib="Wheat etiolated seedling root normalized cDNA
                     library"
                     /tissue_type="Root"
                     /dev_stage="Five day old etiolated seedling"
                     /lab_host="E. coli DH10B"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid
                     pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
                     surface-sterilized, germinated and grown aseptically in
                     the  dark at room temperature on filter paper with water,
                     nystatin and  cefotaxime in covered crystallization
                     dishes. Roots were harvested.  The tissue, total RNA, and
                     poly(A) RNA were prepared, a cDNA library  was made in the
                     TJ Close lab (Choi, Close, Fenton) at the University  of
                     California, Riverside.  The cDNA clones were in vivo
                     excised to  give pBluescript phagemids before
                     normalization was carried out.   The mass excision of
                     phagemid library and normalization were done in HT  Nguyen
                     lab by D. Zhang at Texas Tech Univeristy.  Normalization
                     protocol used was that of Soares.  Plasmid DNA
                     preparations and DNA  sequencing were performed in the OD
                     Anderson lab (all other authors)."
BASE COUNT       84 a    130 c    124 g     84 t
ORIGIN


  Query Match            85.0%;  Score 17;  DB 10;  Length 422;
  Best Local Similarity  100.0%;  Pred. No. 9.2e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggtcggcgagctgatcc 20
          |||||||||||||||||
Db     86 GGTCGGCGAGCTGATCC 102


RESULT   6
BE445100
LOCUS       BE445100                544 bp    mRNA    linear   EST 25-JUL-2000
DEFINITION  WHE1132_H08_P16ZS Wheat etiolated seedling root normalized cDNA
            library Triticum aestivum cDNA clone WHE1132_H08_P16, mRNA
            sequence.
ACCESSION   BE445100
VERSION     BE445100.1  GI:9444655
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 544)
  AUTHORS   Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
            ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
            Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Normalized root cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES             Location/Qualifiers
     source          1. .544
                     /organism="Triticum aestivum"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="WHE1132_H08_P16"
                     /clone_lib="Wheat etiolated seedling root normalized cDNA
                     library"
                     /tissue_type="Root"
                     /dev_stage="Five day old etiolated seedling"
                     /lab_host="E. coli DH10B"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid
                     pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
                     surface-sterilized, germinated and grown aseptically in
                     the  dark at room temperature on filter paper with water,
                     nystatin and  cefotaxime in covered crystallization
                     dishes. Roots were harvested.  The tissue, total RNA, and
                     poly(A) RNA were prepared, a cDNA library  was made in the
                     TJ Close lab (Choi, Close, Fenton) at the University  of
                     California, Riverside.  The cDNA clones were in vivo
                     excised to  give pBluescript phagemids before
                     normalization was carried out.   The mass excision of
                     phagemid library and normalization were done in HT  Nguyen
                     lab by D. Zhang at Texas Tech Univeristy.  Normalization
                     protocol used was that of Soares.  Plasmid DNA
                     preparations and DNA  sequencing were performed in the OD
                     Anderson lab (all other authors)."
BASE COUNT      121 a    173 c    132 g    118 t
ORIGIN


  Query Match            85.0%;  Score 17;  DB 10;  Length 544;
  Best Local Similarity  100.0%;  Pred. No. 9.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggtcggcgagctgatcc 20
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Db    512 GGTCGGCGAGCTGATCC 528
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```
RESULT   7
BE444713
LOCUS       BE444713                558 bp    mRNA    linear   EST 25-JUL-2000
DEFINITION  WHE1137_H03_O05ZS Wheat etiolated seedling root normalized cDNA
            library Triticum aestivum cDNA clone WHE1137_H03_O05, mRNA
            sequence.
ACCESSION   BE444713
VERSION     BE444713.1  GI:9444264
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 558)
  AUTHORS   Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
            ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
            Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Normalized root cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES             Location/Qualifiers
     source          1. .558
                     /organism="Triticum aestivum"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="WHE1137_H03_O05"
                     /clone_lib="Wheat etiolated seedling root normalized cDNA
                     library"
                     /tissue_type="Root"
                     /dev_stage="Five day old etiolated seedling"
                     /lab_host="E. coli DH10B"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid
                     pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
                     surface-sterilized, germinated and grown aseptically in
                     the  dark at room temperature on filter paper with water,
                     nystatin and  cefotaxime in covered crystallization
                     dishes. Roots were harvested.  The tissue, total RNA, and
                     poly(A) RNA were prepared, a cDNA library  was made in the
                     TJ Close lab (Choi, Close, Fenton) at the University  of
                     California, Riverside.  The cDNA clones were in vivo
                     excised to  give pBluescript phagemids before
                     normalization was carried out.   The mass excision of
                     phagemid library and normalization were done in HT  Nguyen
                     lab by D. Zhang at Texas Tech Univeristy.  Normalization
                     protocol used was that of Soares.  Plasmid DNA
                     preparations and DNA  sequencing were performed in the OD
                     Anderson lab (all other authors)."
BASE COUNT      122 a    180 c    134 g    122 t
ORIGIN


  Query Match             85.0%;  Score 17;  DB 10;  Length 558;
  Best Local Similarity   100.0%;  Pred. No. 9.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggtcggcgagctgatcc 20
          |||||||||||||||||
Db    514 GGTCGGCGAGCTGATCC 530


RESULT   8
```

```
BE195103
LOCUS       BE195103                610 bp    mRNA    linear   EST 22-OCT-2001
DEFINITION  HVSMEh0088E21f Hordeum vulgare 5-45 DAP spike EST library
            HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0088E21f,
            mRNA sequence.
ACCESSION   BE195103
VERSION     BE195103.3  GI:16321083
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 610)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
            ,R.D., Close,S.J., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex 5-45 DAP spike cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     On Jun 26, 2000 this sequence version replaced gi:13187931.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 238
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 563.
FEATURES             Location/Qualifiers
     source          1. .610
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEh0088E21f"
                     /clone_lib="Hordeum vulgare 5-45 DAP spike EST library
                     HVcDNA0009 (5 to 45 DAP)"
                     /tissue_type="5-45 DAP Spike"
                     /lab_host="SOLR"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     Plants were grown in the greenhouse at the University of
                     California, Riverside (Fenton, SJ Close, TJ Close). Whole
                     spikes with awns trimmed were collected at 5, 10, 15, 20,
                     30 and 45 DAP (Fenton). Total RNA was prepared from each
                     pool, equal quantities of all six RNA pools were combined,
                     poly(A) RNA was purified from the mixture, one primary
                     unamplified cDNA library was made, and 1 million pfu were
                     in vivo excised to give pBluescript SK(-) cDNA phagemids
                     (Choi)in the TJ Close lab at the University of California,
                     Riverside. Phagemids were plated and picked at the Clemson
                     University Genomics Institute (CUGI) (Begum, Palmer,
                     Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
                     sequencing and sequence analysis were performed at CUGI
                     (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
                     The sequence has been trimmed to remove vector sequence
                     and contains a minimum of 100 bases of phred value 20 or
                     above. For more details on library preparation and
                     sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      127 a    203 c    158 g    120 t      2 others
ORIGIN


  Query Match             85.0%;  Score 17;  DB 9;  Length 610;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy      4 ggtcggcgagctgatcc 20
          ||||||||||||||||
Db    499 GGTCGGCGAGCTGATCC 515


RESULT  9
BE442518
LOCUS       BE442518                658 bp    mRNA    linear   EST 25-JUL-2000
DEFINITION  WHE1101_H10_O19ZS Wheat etiolated seedling root normalized cDNA
            library Triticum aestivum cDNA clone WHE1101_H10_O19, mRNA
            sequence.
ACCESSION   BE442518
VERSION     BE442518.1  GI:9442034
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 658)
  AUTHORS   Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
            ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
            Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Normalized root cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES             Location/Qualifiers
     source          1. .658
                     /organism="Triticum aestivum"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="WHE1101_H10_O19"
                     /clone_lib="Wheat etiolated seedling root normalized cDNA
                     library"
                     /tissue_type="Root"
                     /dev_stage="Five day old etiolated seedling"
                     /lab_host="E. coli DH10B"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid
                     pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
                     surface-sterilized, germinated and grown aseptically in
                     the  dark at room temperature on filter paper with water,
                     nystatin and  cefotaxime in covered crystallization
                     dishes. Roots were harvested.  The tissue, total RNA, and
                     poly(A) RNA were prepared, a cDNA library  was made in the
                     TJ Close lab (Choi, Close, Fenton) at the University  of
                     California, Riverside.  The cDNA clones were in vivo
                     excised to  give pBluescript phagemids before
                     normalization was carried out.  The mass excision of
                     phagemid library and normalization were done in HT  Nguyen
                     lab by D. Zhang at Texas Tech Univeristy.  Normalization
                     protocol used was that of Soares.  Plasmid DNA
                     preparations and DNA  sequencing were performed in the OD
                     Anderson lab (all other authors)."
BASE COUNT      144 a    209 c    165 g    140 t
ORIGIN


  Query Match             85.0%;  Score 17;  DB 10;  Length 658;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggtcggcgagctgatcc 20
          ||||||||||||||||
Db    512 GGTCGGCGAGCTGATCC 528


RESULT  10
BG299722
LOCUS       BG299722                828 bp    mRNA    linear   EST 17-OCT-2001
DEFINITION  HVSMEa0021I20f Hordeum vulgare seedling shoot EST library
            HVcDNA0001 (Cold stress) Hordeum vulgare cDNA clone HVSMEa0021I20f,
            mRNA sequence.
ACCESSION   BG299722
VERSION     BG299722.1  GI:13087434
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 828)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R., Choi,D.W.
            , Fenton,R.D. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Morex cold-stressed seedling shoot cDNA
            library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 574
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 643.
FEATURES             Location/Qualifiers
     source          1. .828
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEa0021I20f"
                     /clone_lib="Hordeum vulgare seedling shoot EST library
                     HVcDNA0001 (Cold stress)"
                     /tissue_type="Seedling shoot"
                     /lab_host="TJC121"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     Seeds were surface sterilized then germinated under axenic
                     conditions in the dark at room temperature on filter paper
                     with water, nystatin and cefotaxime in covered
                     crystallization dishes. Five-day old seedlings were
                     incubated at 5oC for 2 days. Shoots were then harvested,
                     total RNA was prepared, poly(A) RNA was purified, one
                     primary unamplified cDNA library was made, and 600000 pfu
                     were in vivo excised to give pBluescript SK(-) cDNA
                     phagemids. These steps were performed in the TJ Close
                     laboratory at the University of California, Riverside
                     (Choi, Close, Fenton). Phagemids were plated and picked at
                     the Clemson University Genomics Institute (CUGI) (Begum,
                     Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations
                     , DNA sequencing and sequence analysis were performed at
                     CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main
                     ). The sequence has been trimmed to remove vector sequence
                     and contains a minimum of 100 bases of phred value 20 or
                     above. For more details on library preparation and
                     sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      172 a    271 c    220 g    165 t
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ORIGIN


  Query Match             85.0%;  Score 17;  DB 10;  Length 828;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggtcggcgagctgatcc 20
          |||||||||||||||||
Db    500 GGTCGGCGAGCTGATCC 516


RESULT  11
BI188703/c
LOCUS       BI188703                419 bp    mRNA    linear   EST 10-JUL-2001
DEFINITION  d2e05fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
            library Fusarium sporotrichioides cDNA clone d2e05fs 5', mRNA
            sequence.
ACCESSION   BI188703
VERSION     BI188703.1  GI:14662382
KEYWORDS    EST.
SOURCE      Fusarium sporotrichioides.
  ORGANISM  Fusarium sporotrichioides
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; mitosporic Hypocreales; Fusarium.
REFERENCE   1  (bases 1 to 419)
  AUTHORS   Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
            ,M. and Roe,B.
  TITLE     Analysis of a Fusarium sporotrichioides EST database
  JOURNAL   Unpublished (2001)
COMMENT     Other_ESTs: d2e05fs.f1
            Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
            Department of Chemistry and Biochemistry
            Advanced Center for Genome Technology, University of Oklahoma
            620 Parrington Oval, Norman, OK 73019, USA
            Tel: 405 325 4912
            Fax: 405 325 7762
            Email: broe@ou.edu
            Contact Dr. Marian Beremand regarding clone availability Included
            is the best homolog from a blastx search of Genbank nr 04-09-01
            73 2.2 gi|7799258|emb|CAB90 (AL355752) putative integral
            membraneprote
            Seq primer: T3
            High quality sequence stop: 107.
FEATURES             Location/Qualifiers
     source          1. .419
                     /organism="Fusarium sporotrichioides"
                     /strain="Tri 10"
                     /db_xref="taxon:5514"
                     /clone="d2e05fs"
                     /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
                     cDNA library"
                     /note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2:
                     XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
                     ; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT      117 a    106 c    117 g     79 t
ORIGIN


  Query Match             84.0%;  Score 16.8;  DB 10;  Length 419;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||| ||||||| ||||
Db    114 TACGGTCAGCGAGCTCATCC 95


RESULT  12
BI981973/c
LOCUS       BI981973                606 bp    mRNA    linear   EST 24-OCT-2001
DEFINITION  fu53f08.y1 zebrafish adult brain Danio rerio cDNA clone 5333151 5'
            similar to TR:Q9Y4D4 Q9Y4D4 KIAA0648 PROTEIN ;, mRNA sequence.
ACCESSION   BI981973
VERSION     BI981973.1  GI:16371108
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 606)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
            ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
            ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
            Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
            Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
            and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Other_ESTs: fu53f08.x1
            Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
            Matthew Clark. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
            www.rzpd.de)
            High quality sequence stop: 446.
FEATURES             Location/Qualifiers
     source          1. .606
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone="5333151"
                     /clone_lib="zebrafish adult brain"
                     /sex="mixed male and female"
                     /tissue_type="brain"
                     /dev_stage="adult"
                     /lab_host="E. coli DH10B"
                     /note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
                     Original library was constructed in lambdaZIPLOX.  Mass
                     excision of the cDNA library was performed to yield
                     pZIPLOX plasmids. Insert check was done in original
                     library."
BASE COUNT      209 a    133 c    139 g    125 t
ORIGIN


  Query Match             84.0%;  Score 16.8;  DB 10;  Length 606;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          |||||||||||||||| | |
Db    452 TACGGTCGGCGAGCTGTTAC 433


RESULT  13
BI888442/c
LOCUS       BI888442                640 bp    mRNA    linear   EST 12-OCT-2001
DEFINITION  ZF637-2-000197 Zebrafish shield stage whole embryo cDNA library
            MPMGp637 Danio rerio cDNA clone MPMGp637_18E17;MPMGp637E1718 5',
            mRNA sequence.
ACCESSION   BI888442
VERSION     BI888442.1  GI:16095713
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 640)
  AUTHORS   Clark,M., Aanstad,P., Hennig,S., Johnson,S.L. and Lehrach,H.
  TITLE     EST sequencing of a zebrafish shield stage cDNA library normalised
            by oligonucleotide fingerprinting
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Hennig S
            laboraty 123, dept.Lehrach
            Max-Planck-Institut fuer Molekulare Genetik
            Ihnestr.63-73, D-14195 Berlin, Germany
            Tel: +49 30 8413 1612
            Fax: +49 30 8413 1380
            Email: hennig@molgen.mpg.de
            5' EST sequencing of clones from a zebrafish shield stage library,
            normalised from 55,000 starting clones by oligonucleotide
            fingerprinting
            High quality sequence stop: 640.
FEATURES             Location/Qualifiers
     source          1. .640
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone="MPMGp637_18E17;MPMGp637E1718"
                     /clone_lib="Zebrafish shield stage whole embryo cDNA
                     library MPMGp637"
                     /tissue_type="whole embryo"
                     /dev_stage="shield stage, 6 hrs post-fertilisation"
                     /lab_host="E.coli, XL1 blue MRF"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI;
                     oligo-dT-NotI primed, SalI adaptors, directionally cloned,
                     library normalised by oligonucleotide fingerprinting"
BASE COUNT      209 a    152 c    139 g    139 t      1 others
ORIGIN


  Query Match             84.0%;  Score 16.8;  DB 10;  Length 640;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          |||||||||||||||| | |
Db    541 TACGGTCGGCGAGCTGTTAC 522


RESULT  14
AW502654
LOCUS       AW502654                292 bp    mRNA    linear   EST 01-MAR-2000
DEFINITION  UI-HF-BR0p-ajx-b-11-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone
            IMAGE:3075813 5', mRNA sequence.
ACCESSION   AW502654
VERSION     AW502654.1  GI:7117309
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 292)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .292
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3075813"
                     /clone_lib="NIH_MGC_52"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (7.4-9.5kb).  Directionally cloned. Cells provided by
                     Louis M. Staudt, Ph.D.  Library preparation by Maria de
                     Fatima Bonaldo, Ph.D. and  M. Bento Soares, Ph.D. "
BASE COUNT       51 a     84 c    105 g     52 t
ORIGIN


  Query Match             82.0%;  Score 16.4;  DB 9;  Length 292;
  Best Local Similarity   94.4%;  Pred. No. 1.6e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 acggtcggcgagctgatc 19
          |||||||||| |||||||
Db     46 ACGGTCGGCGTGCTGATC 63


RESULT  15
AW501791
LOCUS       AW501791                338 bp    mRNA    linear   EST 01-MAR-2000
DEFINITION  UI-HF-BR0p-ajm-g-11-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone
            IMAGE:3075260 5', mRNA sequence.
ACCESSION   AW501791
VERSION     AW501791.1  GI:7115654
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 338)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .338
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3075260"
                     /clone_lib="NIH_MGC_52"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (7.4-9.5kb).  Directionally cloned. Cells provided by
                     Louis M. Staudt, Ph.D.  Library preparation by Maria de
                     Fatima Bonaldo, Ph.D. and  M. Bento Soares, Ph.D. "
BASE COUNT       56 a     98 c    124 g     60 t
ORIGIN


  Query Match             82.0%;  Score 16.4;  DB 9;  Length 338;
```

Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2 acggtcggcgagctgatc 19
           ||||||||| |||||||
Db      46 ACGGTCGGCGTGCTGATC 63
```

Search completed: August 7, 2002, 21:15:17
Job time: 22887 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 15:13:45 ; Search time 2167.9 Seconds
(without alignments)
193.058 Million cell updates/sec

Title: US-09-786-105-1
Perfect score: 20
Sequence: 1 tacggtcggcgagctgatcc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	20	100.0	306	1	AF057450	AF057450 Mycobacte
2	20	100.0	306	1	AF057451	AF057451 Mycobacte
3	20	100.0	306	1	AF057452	AF057452 Mycobacte
4	20	100.0	306	1	AF057453	AF057453 Mycobacte
5	20	100.0	306	1	AF057454	AF057454 Mycobacte
6	20	100.0	306	6	AR157003	AR157003 Sequence
7	20	100.0	306	6	AR157007	AR157007 Sequence
8	20	100.0	306	6	AR157008	AR157008 Sequence
9	20	100.0	306	6	AR157042	AR157042 Sequence
10	20	100.0	306	6	AR157051	AR157051 Sequence
11	20	100.0	432	1	MSGRIFRNAP	L05910 Mycobacteri
12	20	100.0	432	6	AR067448	AR067448 Sequence
13	20	100.0	970	6	I50706	I50706 Sequence 1
14	20	100.0	3534	6	AX111339	AX111339 Sequence
15	20	100.0	3853	1	MTU12205	U12205 Mycobacteri
16	20	100.0	5084	1	MSGRPOB	L27989 Mycobacteri
17	20	100.0	19352	1	AE006964	AE006964 Mycobacte
18	20	100.0	19770	1	MTCI376	Z95972 Mycobacteri
19	19	95.0	306	1	AF057493	AF057493 Mycobacte
20	19	95.0	306	6	AR157045	AR157045 Sequence
21	18.4	92.0	25	6	A47816	A47816 Sequence 30
22	18.4	92.0	306	1	AF057456	AF057456 Mycobacte
23	18.4	92.0	306	1	AF057459	AF057459 Mycobacte
24	18.4	92.0	306	1	AF057460	AF057460 Mycobacte
25	18.4	92.0	306	1	AF057471	AF057471 Mycobacte
26	18.4	92.0	306	1	AF057473	AF057473 Mycobacte
27	18.4	92.0	306	1	AF057496	AF057496 Corynebac
28	18.4	92.0	306	1	AF173087	AF173087 Mycobacte
29	18.4	92.0	306	6	AR157005	AR157005 Sequence
30	18.4	92.0	306	6	AR157010	AR157010 Sequence
31	18.4	92.0	306	6	AR157011	AR157011 Sequence
32	18.4	92.0	306	6	AR157021	AR157021 Sequence
33	18.4	92.0	306	6	AR157024	AR157024 Sequence
34	18.4	92.0	306	6	AR157046	AR157046 Sequence
c 35	18	90.0	87	6	AX050338	AX050338 Sequence
36	17.4	87.0	306	1	AF057463	AF057463 Mycobacte
37	17.4	87.0	306	1	AF057466	AF057466 Mycobacte
38	17.4	87.0	306	1	AF057475	AF057475 Mycobacte
39	17.4	87.0	306	1	AF057480	AF057480 Mycobacte
40	17.4	87.0	306	1	AF057489	AF057489 Mycobacte
41	17.4	87.0	306	1	AF057492	AF057492 Mycobacte
42	17.4	87.0	306	1	AF057494	AF057494 Rhodococc
43	17.4	87.0	306	1	AF057495	AF057495 Nocardia
44	17.4	87.0	306	1	AF173084	AF173084 Mycobacte
45	17.4	87.0	306	1	AF173086	AF173086 Mycobacte

ALIGNMENTS

RESULT 1
AF057450
LOCUS AF057450 306 bp DNA linear BCT 17-SEP-1999
DEFINITION Mycobacterium africanum RNA polymerase beta (rpoB) gene, partial cds.
ACCESSION AF057450
VERSION AF057450.1 GI:5902487
KEYWORDS .
SOURCE Mycobacterium africanum.
ORGANISM Mycobacterium africanum
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T., Kim,E.C., Cha,C.Y. and Kook,Y.H.
TITLE Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)
JOURNAL J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
MEDLINE 99262756
PUBMED 10325313
REFERENCE 2 (bases 1 to 306)
AUTHORS Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,

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            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
     source          1. .306
                     /organism="Mycobacterium africanum"
                     /strain="ATCC25420"
                     /db_xref="ATCC:25420"
                     /db_xref="taxon:33894"
     gene            <1. .>306
                     /gene="rpoB"
     CDS             <1. .>306
                     /gene="rpoB"
                     /codon_start=3
                     /transl_table=11
                     /product="RNA polymerase beta"
                     /protein_id="AAD55514.1"
                     /db_xref="GI:5902488"
                     /translation="RTVGELIQNQIRVGMSRMERVVRERMTTQDVEAITPQTLINIRP
                     VVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDVHPSH"
BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 1;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   2
AF057451
LOCUS       AF057451                306 bp    DNA     linear   BCT 17-SEP-1999
DEFINITION  Mycobacterium bovis RNA polymerase beta (rpoB) gene, partial cds.
ACCESSION   AF057451
VERSION     AF057451.1  GI:5902489
KEYWORDS    .
SOURCE      Mycobacterium bovis.
  ORGANISM  Mycobacterium bovis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
  MEDLINE   99262756
   PUBMED   10325313
REFERENCE   2  (bases 1 to 306)
  AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
     source          1. .306
                     /organism="Mycobacterium bovis"
                     /strain="ATCC19210"
                     /db_xref="ATCC:19210"
                     /db_xref="taxon:1765"
     gene            <1. .>306
                     /gene="rpoB"
     CDS             <1. .>306
                     /gene="rpoB"
                     /codon_start=3
                     /transl_table=11
                     /product="RNA polymerase beta"
                     /protein_id="AAD55515.1"
                     /db_xref="GI:5902490"
                     /translation="RTVGELIQNQIRVGMSRMERVVRERMTTQDVEAITPQTLINIRP
                     VVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDVHPSH"
BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 1;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   3
AF057452
LOCUS       AF057452                306 bp    DNA     linear   BCT 17-SEP-1999
DEFINITION  Mycobacterium bovis BCG strain French 1173P2 RNA polymerase beta
            (rpoB) gene, partial cds.
ACCESSION   AF057452
VERSION     AF057452.1  GI:5902491
KEYWORDS    .
SOURCE      Mycobacterium bovis BCG.
  ORGANISM  Mycobacterium bovis BCG
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
  MEDLINE   99262756
   PUBMED   10325313
REFERENCE   2  (bases 1 to 306)
  AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
     source          1. .306
                     /organism="Mycobacterium bovis BCG"
                     /strain="French 1173P2"
                     /db_xref="taxon:33892"
     gene            <1. .>306
                     /gene="rpoB"
     CDS             <1. .>306
                     /gene="rpoB"
                     /codon_start=3
                     /transl_table=11
                     /product="RNA polymerase beta"
                     /protein_id="AAD55516.1"
                     /db_xref="GI:5902492"
                     /translation="RTVGELIQNQIRVGMSRMERVVRERMTTQDVEAITPQTLINIRP
                     VVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDVHPSH"
BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 1;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
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Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   4
AF057453
LOCUS       AF057453                306 bp    DNA     linear   BCT 17-SEP-1999
DEFINITION  Mycobacterium bovis BCG RNA polymerase beta (rpoB) gene, partial
            cds.
ACCESSION   AF057453
VERSION     AF057453.1  GI:5902493
KEYWORDS    .
SOURCE      Mycobacterium bovis BCG.
  ORGANISM  Mycobacterium bovis BCG
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
  MEDLINE   99262756
   PUBMED   10325313
REFERENCE   2  (bases 1 to 306)
  AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
     source          1. .306
                     /organism="Mycobacterium bovis BCG"
                     /strain="Tokyo T172"
                     /db_xref="taxon:33892"
     gene            <1. .>306
                     /gene="rpoB"
     CDS             <1. .>306
                     /gene="rpoB"
                     /codon_start=3
                     /transl_table=11
                     /product="RNA polymerase beta"
                     /protein_id="AAD55517.1"
                     /db_xref="GI:5902494"
                     /translation="RTVGELIQNQIRVGMSRMERVVRERMTTQDVEAITPQTLINIRP
                     VVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDVHPSH"
BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


  Query Match           100.0%;  Score 20;  DB 1;  Length 306;
  Best Local Similarity  100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   5
AF057454
LOCUS       AF057454                306 bp    DNA     linear   BCT 08-OCT-1999
DEFINITION  Mycobacterium tuberculosis RNA polymerase beta (rpoB) gene, partial
            cds.
ACCESSION   AF057454
VERSION     AF057454.1  GI:5902495
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
  TITLE     Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
  JOURNAL   J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
  MEDLINE   99262756
   PUBMED   10325313
REFERENCE   2  (bases 1 to 306)
  AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES             Location/Qualifiers
     source          1. .306
                     /organism="Mycobacterium tuberculosis"
                     /strain="H37Rv; ATCC27294"
                     /db_xref="ATCC:27294"
                     /db_xref="taxon:1773"
     gene            <1. .>306
                     /gene="rpoB"
     CDS             <1. .>306
                     /gene="rpoB"
                     /codon_start=3
                     /transl_table=11
                     /product="RNA polymerase beta"
                     /protein_id="AAD55518.1"
                     /db_xref="GI:5902496"
                     /translation="RTVGELIQNQIRVGMSRMERVVRERMTTQDVEAITPQTLINIRP
                     VVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDVHPSH"
BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


  Query Match           100.0%;  Score 20;  DB 1;  Length 306;
  Best Local Similarity  100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   6
AR157003
LOCUS       AR157003                306 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6242584.
ACCESSION   AR157003
VERSION     AR157003.1  GI:15125707
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kook,Y. and Kim,B.
  TITLE     Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
  JOURNAL   Patent: US 6242584-A 2 05-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .306
                     /organism="unknown"
BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


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  Best Local Similarity  100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
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Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   7
AR157007
LOCUS       AR157007                306 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 6 from patent US 6242584.
ACCESSION   AR157007
VERSION     AR157007.1  GI:15125711
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kook,Y.-H. and Kim,B.-J.
  TITLE     Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
  JOURNAL   Patent: US 6242584-A 6 05-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .306
                     /organism="unknown"
BASE COUNT       56 a     96 c    107 g     47 t
ORIGIN


  Query Match            100.0%;  Score 20;  DB 6;  Length 306;
  Best Local Similarity  100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   8
AR157008
LOCUS       AR157008                306 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 7 from patent US 6242584.
ACCESSION   AR157008
VERSION     AR157008.1  GI:15125712
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kook,Y. and Kim,B.
  TITLE     Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
  JOURNAL   Patent: US 6242584-A 7 05-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .306
                     /organism="unknown"
BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


  Query Match            100.0%;  Score 20;  DB 6;  Length 306;
  Best Local Similarity  100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT   9
AR157042
LOCUS       AR157042                306 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 41 from patent US 6242584.
ACCESSION   AR157042
VERSION     AR157042.1  GI:15125746
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kook,Y. and Kim,B.
  TITLE     Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
  JOURNAL   Patent: US 6242584-A 41 05-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .306
                     /organism="unknown"
BASE COUNT       56 a     95 c    108 g     47 t
ORIGIN


  Query Match            100.0%;  Score 20;  DB 6;  Length 306;
  Best Local Similarity  100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT  10
AR157051
LOCUS       AR157051                306 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 50 from patent US 6242584.
ACCESSION   AR157051
VERSION     AR157051.1  GI:15125755
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 306)
  AUTHORS   Kook,Y. and Kim,B.
  TITLE     Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
  JOURNAL   Patent: US 6242584-A 50 05-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .306
                     /organism="unknown"
BASE COUNT       56 a     94 c    108 g     48 t
ORIGIN


  Query Match            100.0%;  Score 20;  DB 6;  Length 306;
  Best Local Similarity  100.0%;  Pred. No. 96;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
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Db      5 TACGGTCGGCGAGCTGATCC 24


RESULT  11
MSGRIFRNAP
LOCUS       MSGRIFRNAP              432 bp    DNA     linear   BCT 21-MAY-1993
DEFINITION  Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin
            resistance gene, complete cds.
ACCESSION   L05910
VERSION     L05910.1  GI:149991
KEYWORDS    RNA polymerase beta-subunit; rifampicin resistance.
SOURCE      Mycobacterium tuberculosis (strain H37) DNA.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 432)
  AUTHORS   Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T.,
            Colston,J., Matter,L., Schopfer,K. and Bodmer,T.
  TITLE     Detection of rifampicin-resistance mutation in Mycobacterium
            tuberculosis
  JOURNAL   Antimicrob. Agents Chemother. 341, 647-650 (1993)
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FEATURES             Location/Qualifiers
     source          1. .432
                     /organism="Mycobacterium tuberculosis"
                     /strain="H37"
                     /db_xref="taxon:1773"
     CDS             <1. .>432
                     /codon_start=1
                     /transl_table=11
                     /product="RNA polymerase beta subunit"
                     /protein_id="AAB59068.1"
                     /db_xref="GI:149992"
                     /translation="GNRRLRTVGELIQNQIRVGMSRMERVVRERMTTQDVEAITPQTL
                     INIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDV
                     HPSHYGRMCPIETPEGPNIGLIGSLSVYARVNPFGFIETPYR"
     variation       149
                     /phenotype="rifampicin resistant in association with
                     mutation 234 G"
                     /replace="c"
     variation       188
                     /phenotype="rifampicin resistant"
                     /replace="c"
     variation       191
                     /phenotype="rifampicin resistant in association with
                     mutation 203 T"
                     /replace="c"
     variation       194
                     /phenotype="rifampicin resistant"
                     /replace="t"
     variation       203
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                     /replace="t"
     variation       208. .210
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                     /replace="g"
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                     /replace="c"
BASE COUNT       77 a    140 c    148 g     67 t
ORIGIN


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  Best Local Similarity  100.0%;  Pred. No. 94;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db     18 TACGGTCGGCGAGCTGATCC 37
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RESULT  12
AR067448
LOCUS       AR067448                 432 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 59 from patent US 5851763.
ACCESSION   AR067448
VERSION     AR067448.1  GI:5998670
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 432)
  AUTHORS   Heym,B., Cole,S., Young,D., Zhang,Y., Honore,N., Telenti,A. and
            Bodmer,T.
  TITLE     Rapid detection of antibiotic resistance in mycobacterium
            tuberculosis
  JOURNAL   Patent: US 5851763-A 59 22-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .432
                     /organism="unknown"
BASE COUNT       77 a    139 c    149 g     67 t
ORIGIN


  Query Match           100.0%;  Score 20;  DB 6;  Length 432;
  Best Local Similarity  100.0%;  Pred. No. 94;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db     18 TACGGTCGGCGAGCTGATCC 37


RESULT  13
I50706
LOCUS       I50706                   970 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1 from patent US 5643723.
ACCESSION   I50706
VERSION     I50706.1  GI:2472409
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 970)
  AUTHORS   Persing,D.H., Hunt,J.J., Young,K.K.Y., Felmlee,T.A., Roberts,G.D.
            and Whelan,A.Christian.
  TITLE     Detection of a genetic locus encoding resistance to rifampin in
            mycobacterial cultures and in clinical specimens
  JOURNAL   Patent: US 5643723-A 1 01-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .970
                     /organism="unknown"
BASE COUNT      182 a    302 c    330 g    156 t
ORIGIN


  Query Match           100.0%;  Score 20;  DB 6;  Length 970;
  Best Local Similarity  100.0%;  Pred. No. 88;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db    261 TACGGTCGGCGAGCTGATCC 280


RESULT  14
AX111339
LOCUS       AX111339                3534 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 2072 from Patent WO0123604.
ACCESSION   AX111339
VERSION     AX111339.1  GI:13927631
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
```

```
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 3534)
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 2072 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .3534
                     /organism="Mycobacterium tuberculosis"
                     /strain="Rv"
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BASE COUNT      679 a   1081 c   1188 g    586 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 6;  Length 3534;
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Qy      1 tacggtcggcgagctgatcc 20
          ||||||||||||||||||||
Db   1137 TACGGTCGGCGAGCTGATCC 1156


RESULT  15
MTU12205
LOCUS       MTU12205                3853 bp    DNA     linear   BCT 02-MAR-2000
DEFINITION  Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
            gene, partial cds.
ACCESSION   U12205
VERSION     U12205.1  GI:515684
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis.
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE   1  (bases 1 to 3853)
  AUTHORS   Imboden,P., Troller,R., Marchesi,F., Telenti,A., Bodmer,T.,
            Cole,S., Schopfer,K. and Burkart,T.
  TITLE     The rpoB gene of Mycobacterium tuberculosis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3853)
  AUTHORS   Imboden,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-1994) Paul Imboden, Institute for Medical
            Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
            3010, Switzerland
FEATURES             Location/Qualifiers
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                     /strain="H37Rv"
                     /db_xref="taxon:1773"
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                     /gene="rpoB"
     CDS             576. .>3853
                     /gene="rpoB"
                     /codon_start=1
                     /transl_table=11
                     /product="RNA-polymerase beta subunit"
                     /protein_id="AAA20242.2"
                     /db_xref="GI:7144499"
                     /translation="MLEGCILADSRQSKTAASPSPSRPQSSSNNSVPGAPNRVSFAKL
                     REPLEVPGLLDVQTDSFEWLIGSPRWRESAAERGDVNPVGGLEEVLYELSPIEDFSGS
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                     TEKGTFIINGTERVVVSQLVRSPGVYFDETIDKSTDKTLHSVKVIPSRGAWLEFDVDK
                     RDTVGVRIDRKRRQPVTVLLKALGWTSEQIVERFGFSEIMRSTLEKDNTVGTDEALLD
                     IYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARVGRYKVNKKLGLHVGEPITSSTLT
                     EEDVVATIEYLVRLHEGQTTMTVPGGVEVPVETDDIDHFGNRRLRTVGELIQNQIRVG
                     MSRMERVVRERMTTQDVEAITPQTLINIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLT
                     HKRRLSALGPGGLSRERAGLEVRDVHPSHYGRMCPIETPEGPNIGLIGSLSVYARVNP
                     FGFIETPYRKVVDGVVSDGIVYLTADEEDRHVVAQANSPIDADGRFVEPRVLVRRKAG
                     EVEYVPSSEVDYMDVSPRQMVSVATAMIPFLEHDDANRALMGANMQRQAVPLVRSEAP
                     LVGTGMELRAAIDAATSSSQESGVIEEVSADYITVMHDNGTRRTYRMRKFARSNHGTC
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                     VEEDVLTSIHIEEHEIDARDTKLGAEEITRDIPNISDEVLADLDERGIVRIGAEVRDG
                     DILVGKVTPKGETELTPEERLLRAIFGEKAREVRDTSLKVPHGESGKVIGIRVFSRED
                     EDELPAGVNELVRVYVAQKRKISDGDKLAGRHGNKGVIGKILPVEDMPFLADGTPVDI
                     ILNTHGVPRRMNIGQILETHLGWCAHSGWKVDAAKGVPDWAARLPDELLEAQPNAIVS
                     TPVFDGAQEAELQGLLSCTLPNRDGDVLVDADGKAMLFDGRSGEPFPYPVTVGYMYIM
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                     TIKS"
BASE COUNT      723 a   1173 c   1293 g    664 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 1;  Length 3853;
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Job time: 23872 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:54:31 ; Search time 562.71 Seconds
(without alignments)
61.023 Million cell updates/sec

Title: US-09-786-105-1
Perfect score: 20
Sequence: 1 tacggtcggcgagctgatcc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

ord size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query Match	Length	DB	ID	Description
	1	20	100.0	20	17	AAT12092	M. tuberculosis rp
	2	20	100.0	20	21	AAA49823	Mycobacterium tube
	3	20	100.0	20	21	AAA49825	Mycobacterium tube
	4	20	100.0	306	19	AAX27214	RpoB gene fragment
	5	20	100.0	306	19	AAX27175	RpoB gene fragment
	6	20	100.0	306	19	AAX27179	RpoB gene fragment
	7	20	100.0	306	19	AAX27180	RpoB gene fragment
	8	20	100.0	306	24	AAS99526	Mycobacterium spec
	9	20	100.0	306	24	AAS99527	Mycobacterium spec
	10	20	100.0	306	24	AAS99530	Mycobacterium spec
	11	20	100.0	306	24	AAS99531	Mycobacterium spec
	12	20	100.0	432	14	AAQ61457	M.tuberculosis rpo
	13	20	100.0	480	21	AAA49863	Mycobacterium tube
	14	20	100.0	970	17	AAT09676	Mycobacterium tube
	15	20	100.0	3519	22	AAH51976	Mycobacterium tube
	16	20	100.0	3534	22	AAH02079	Mycobacterium tube
	17	20	100.0	3853	21	AAA74651	Mycobacterium tube
	18	20	100.0	3853	21	AAA89994	M. tuberculosis rp
	19	19	95.0	306	19	AAX27217	RpoB gene fragment
	20	19	95.0	306	24	AAS99551	Mycobacterium spec
	21	19	95.0	21500	23	AAS59633	Propionibacterium
	22	18	90.0	25	17	AAT12091	M. tuberculosis rp
c	23	18	90.0	87	22	AAC88922	Mycobacterium tube
	24	16	80.0	306	19	AAX27212	RpoB gene fragment
	25	16	80.0	306	19	AAX27218	RpoB gene fragment
	26	16	80.0	306	19	AAX27193	RpoB gene fragment
	27	16	80.0	306	19	AAX27196	RpoB gene fragment
	28	16	80.0	306	19	AAX27204	RpoB gene fragment
	29	16	80.0	306	19	AAX27177	RpoB gene fragment
	30	16	80.0	306	19	AAX27182	RpoB gene fragment
	31	16	80.0	306	19	AAX27183	RpoB gene fragment
	32	16	80.0	306	19	AAX27186	RpoB gene fragment
	33	16	80.0	306	24	AAS99539	Mycobacterium spec
	34	16	80.0	306	24	AAS99557	Mycobacterium spec
	35	16	80.0	306	24	AAS99560	Mycobacterium spec
	36	16	80.0	306	24	AAS99565	Mycobacterium spec
	37	16	80.0	306	24	AAS99568	Mycobacterium spec
	38	16	80.0	27426	23	AAS59541	Propionibacterium
	39	15	75.0	1092	22	AAS02316	B. subtilis DNA en
	40	15	75.0	2488	23	ABL14021	Drosophila melanog
	41	15	75.0	2772	23	AAS54170	Pseudomonas aerugi
c	42	15	75.0	4544	23	ABL14020	Drosophila melanog
	43	15	75.0	4403765	22	AAI99683	Mycobacterium tube
	44	15	75.0	4411529	22	AAI99682	Mycobacterium tube
	45	14	70.0	50	19	AAV31045	Expression vector

ALIGNMENTS

RESULT 1
AAT12092
ID AAT12092 standard; DNA; 20 BP.
XX
AC AAT12092;
XX
DT 10-JUL-1996 (first entry)
XX
DE M. tuberculosis rpoB gene fragment amplification primer P2.
XX
KW Antibiotic; resistance; spectrum; gene; mycobacterium;
KW determination; amplification; tuberculosis; rpoB; fragment;
KW primer; differential; hybridisation; pattern; rifampicin;
KW rifabutin; species identification; ss.
XX
OS Synthetic.
XX
PN [redacted]
XX
PD 14-DEC-1995.
XX
PF 09-JUN-1995; 95WO-EP02230.
XX
PR 09-JUN-1994; 94EP-0870093.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI De Beenhouwer H, Jannes G, Machtelinckx L, Portaels F;
PI Rossau R;
XX
DR WPI; 1996-040250/04.
XX

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PT Probes and primers for determn. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene
XX
PS Claim 22; Page 39; 69pp; English.
XX
CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT12091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrids formed and
CC inferring the ARS, and opt. the spp., from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampicin and/or rifabutin resistance in M. leprae
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determn.
CC of ARS and spp. identity.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 tacggtcggcgagctgatcc 20

RESULT 2
AAA49823
ID AAA49823 standard; DNA; 20 BP.
XX
AC AAA49823;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene amplification primer rpoB-F.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 4; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene amplification primer rpoB-F (bp
CC 2201-2220). It is used with the reverse primer given in AAA49824
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 tacggtcggcgagctgatcc 20

RESULT 3
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ID AAA49825 standard; DNA; 20 BP.
XX
AC AAA49825;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-5s.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene sequencing primer rpoB-5s (bp
CC 2201-2220). It is used with the reverse primer given in AAA49826 and
CC with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.

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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 22:04:01 ; Search time 568.44 Seconds
(without alignments)
60.408 Million cell updates/sec

Title: US-09-786-105-3
Perfect score: 20
Sequence: 1 tacggtcggcgagctgatcc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*
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5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
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24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	17	AAT12092	M. tuberculosis rp
2	20	100.0	20	21	AAA49823	Mycobacterium tube
3	20	100.0	20	21	AAA49825	Mycobacterium tube
4	20	100.0	306	19	AAX27214	RpoB gene fragment
5	20	100.0	306	19	AAX27175	RpoB gene fragment
6	20	100.0	306	19	AAX27179	RpoB gene fragment
7	20	100.0	306	19	AAX27180	RpoB gene fragment
8	20	100.0	306	24	AAS99526	Mycobacterium spec
9	20	100.0	306	24	AAS99527	Mycobacterium spec
10	20	100.0	306	24	AAS99530	Mycobacterium spec
11	20	100.0	306	24	AAS99531	Mycobacterium spec
12	20	100.0	432	14	AAQ61457	M.tuberculosis rpo
13	20	100.0	480	21	AAA49863	Mycobacterium tube
14	20	100.0	970	17	AAT09676	Mycobacterium tube
15	20	100.0	3519	22	AAH51976	Mycobacterium tube
16	20	100.0	3534	22	AAH02079	Mycobacterium tube
17	20	100.0	3853	21	AAA74651	Mycobacterium tube
18	20	100.0	3853	21	AAA89994	M. tuberculosis rp
19	19	95.0	306	19	AAX27217	RpoB gene fragment
20	19	95.0	306	24	AAS99551	Mycobacterium spec
21	19	95.0	21500	23	AAS59633	Propionibacterium
22	18.4	92.0	25	17	AAT12091	M. tuberculosis rp
23	18.4	92.0	306	19	AAX27218	RpoB gene fragment
24	18.4	92.0	306	19	AAX27193	RpoB gene fragment
25	18.4	92.0	306	19	AAX27196	RpoB gene fragment
26	18.4	92.0	306	19	AAX27177	RpoB gene fragment
27	18.4	92.0	306	19	AAX27182	RpoB gene fragment
28	18.4	92.0	306	19	AAX27183	RpoB gene fragment
29	18.4	92.0	306	24	AAS99539	Mycobacterium spec
30	18.4	92.0	306	24	AAS99557	Mycobacterium spec
31	18.4	92.0	27426	23	AAS59541	Propionibacterium
c 32	18	90.0	87	22	AAC88922	Mycobacterium tube
33	17.4	87.0	306	19	AAX27212	RpoB gene fragment
34	17.4	87.0	306	19	AAX27216	RpoB gene fragment
35	17.4	87.0	306	19	AAX27219	RpoB gene fragment
36	17.4	87.0	306	19	AAX27220	RpoB gene fragment
37	17.4	87.0	306	19	AAX27198	RpoB gene fragment
38	17.4	87.0	306	19	AAX27204	RpoB gene fragment
39	17.4	87.0	306	19	AAX27186	RpoB gene fragment
40	17.4	87.0	306	19	AAX27189	RpoB gene fragment
41	17.4	87.0	306	24	AAS99534	Mycobacterium spec
42	17.4	87.0	306	24	AAS99543	Mycobacterium spec
43	17.4	87.0	306	24	AAS99560	Mycobacterium spec
44	17.4	87.0	306	24	AAS99565	Mycobacterium spec
45	17.4	87.0	306	24	AAS99568	Mycobacterium spec

ALIGNMENTS

RESULT 1
AAT12092
ID AAT12092 standard; DNA; 20 BP.
XX
AC AAT12092;
XX
DT 10-JUL-1996 (first entry)
XX
DE M. tuberculosis rpoB gene fragment amplification primer P2.
XX
KW Antibiotic; resistance; spectrum; gene; mycobacterium;
KW determination; amplification; tuberculosis; rpoB; fragment;
KW primer; differential; hybridisation; pattern; rifampicin;
KW rifabutin; species identification; ss.
XX
OS Synthetic.
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PN [redacted]
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PD 14-DEC-1995.
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PF 09-JUN-1995; 95WO-EP02230.
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PR 09-JUN-1994; 94EP-0870093.
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PA (INNO-) INNOGENETICS NV.
XX
PI De Beenhouwer H, Jannes G, Machtelinckx L, Portaels F;
PI Rossau R;
XX
DR WPI; 1996-040250/04.
XX

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PT Probes and primers for determn. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene
XX
PS Claim 22; Page 39; 69pp; English.
XX
CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT12091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrids formed and
CC inferring the ARS, and opt. the spp., from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampicin and/or rifabutin resistance in M. leprae
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determn.
CC of ARS and spp. identity.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 tacggtcggcgagctgatcc 20

RESULT 2
AAA49823
ID AAA49823 standard; DNA; 20 BP.
XX
AC AAA49823;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene amplification primer rpoB-F.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 4; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene amplification primer rpoB-F (bp
CC 2201-2220). It is used with the reverse primer given in AAA49824
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

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Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ID AAA49825 standard; DNA; 20 BP.
XX
AC AAA49825;
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DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-5s.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene sequencing primer rpoB-5s (bp
CC 2201-2220). It is used with the reverse primer given in AAA49826 and
CC with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.

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GenCore version 4.5

OM nucleic - nucleic search, using sw model

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(without alignments)
33.266 Million cell updates/sec

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Perfect score: 20
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query Match	Length	DB	ID	Description
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c	2	20	100.0	432	3	US-09-082-614A-59	Sequence 59, Appl
c	3	20	100.0	620	2	US-08-757-653-135	Sequence 135, App
c	4	20	100.0	620	2	US-08-757-653-136	Sequence 136, App
c	5	20	100.0	620	2	US-08-757-653-137	Sequence 137, App
	6	20	100.0	620	2	US-08-757-653-138	Sequence 138, App
	7	20	100.0	620	2	US-08-757-653-139	Sequence 139, App
	8	20	100.0	620	2	US-08-757-653-140	Sequence 140, App
c	9	20	100.0	706	4	US-08-797-812-24	Sequence 24, Appl
c	10	20	100.0	970	1	US-08-250-030-1	Sequence 1, Appli
c	11	20	100.0	970	5	PCT-US95-06790-1	Sequence 1, Appli
	12	19	95.0	19	4	US-08-750-088A-71	Sequence 71, Appl
	13	15	75.0	27	1	US-08-250-030-9	Sequence 9, Appli
	14	15	75.0	27	5	PCT-US95-06790-9	Sequence 9, Appli
c	15	14	70.0	3447	2	US-08-313-185-57	Sequence 57, Appl
c	16	14	70.0	3447	3	US-09-082-614A-57	Sequence 57, Appl
	17	13	65.0	383	3	US-08-906-769-169	Sequence 169, App
	18	13	65.0	383	3	US-08-906-616-169	Sequence 169, App
	19	13	65.0	383	3	US-08-639-075A-169	Sequence 169, App
	20	13	65.0	383	4	US-09-012-431-169	Sequence 169, App
	21	13	65.0	383	4	US-09-012-692-169	Sequence 169, App
	22	13	65.0	383	4	US-08-906-613-169	Sequence 169, App
	23	13	65.0	537	3	US-08-906-769-171	Sequence 171, App
	24	13	65.0	537	3	US-08-906-616-171	Sequence 171, App
	25	13	65.0	537	3	US-08-639-075A-171	Sequence 171, App
	26	13	65.0	537	4	US-09-012-431-171	Sequence 171, App
	27	13	65.0	537	4	US-09-012-692-171	Sequence 171, App
	28	13	65.0	537	4	US-08-906-613-171	Sequence 171, App
	29	13	65.0	1938	4	US-09-232-200-29	Sequence 29, Appl
	30	13	65.0	1938	4	US-09-232-197-29	Sequence 29, Appl
	31	13	65.0	1938	4	US-09-232-201-29	Sequence 29, Appl
c	32	13	65.0	3000	2	US-08-896-344A-1	Sequence 1, Appli
c	33	13	65.0	3000	4	US-09-360-682A-1	Sequence 1, Appli
	34	13	65.0	3217	4	US-09-232-200-64	Sequence 64, Appl
	35	13	65.0	3217	4	US-09-232-197-64	Sequence 64, Appl
	36	13	65.0	3217	4	US-09-232-201-64	Sequence 64, Appl
c	37	13	65.0	4403765	4	US-09-103-840A-2	Sequence 2, Appli
	38	12	60.0	391	1	US-08-636-928-6	Sequence 6, Appli
	39	12	60.0	412	4	US-08-976-259-123	Sequence 123, App
c	40	12	60.0	645	1	US-08-459-586-19	Sequence 19, Appl
c	41	12	60.0	645	2	US-08-282-696-19	Sequence 19, Appl
	42	12	60.0	648	5	PCT-US96-04648-4	Sequence 4, Appli
c	43	12	60.0	709	1	US-08-459-586-20	Sequence 20, Appl
c	44	12	60.0	709	2	US-08-282-696-20	Sequence 20, Appl
c	45	12	60.0	728	4	US-08-998-416-615	Sequence 615, App

ALIGNMENTS

RESULT 1
US-08-313-185-59/c
; Sequence 59, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-59

Query Match 100.0%; Score 20; DB 2; Length 432;

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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db     428 TACGGCGTTTCGATGAACCC 409


RESULT   2
US-09-082-614A-59/c
; Sequence 59, Application US/09082614A
; Patent No. 6124098
;  GENERAL INFORMATION:
;    APPLICANT:  Heym, Beate
;    APPLICANT:  Cole, Stewart
;    APPLICANT:  Young, Douglas
;    APPLICANT:  Zhang, Ying
;    APPLICANT:  Honore, Nadine
;    APPLICANT:  Telenti, Amalio
;    APPLICANT:  Bodmer, Thomas
;    TITLE OF INVENTION:  Rapid Detection of Antibiotic Resistance
;    TITLE OF INVENTION:  in Mycobacterium Tuberculosis
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/082,614A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/313,185
;      FILING DATE:  12-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  02356.0068-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-082-614A-59


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RESULT   3
US-08-757-653-135/c
; Sequence 135, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  135:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-135


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; Sequence 136, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

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Perfect score: 20
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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c	10	20	100.0	970	1	US-08-250-030-1	Sequence 1, Appli
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	14	15	75.0	27	5	PCT-US95-06790-9	Sequence 9, Appli
c	15	14	70.0	3447	2	US-08-313-185-57	Sequence 57, Appl
c	16	14	70.0	3447	3	US-09-082-614A-57	Sequence 57, Appl
	17	13	65.0	383	3	US-08-906-769-169	Sequence 169, App
	18	13	65.0	383	3	US-08-906-616-169	Sequence 169, App
	19	13	65.0	383	3	US-08-639-075A-169	Sequence 169, App
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	21	13	65.0	383	4	US-09-012-692-169	Sequence 169, App
	22	13	65.0	383	4	US-08-906-613-169	Sequence 169, App
	23	13	65.0	537	3	US-08-906-769-171	Sequence 171, App
	24	13	65.0	537	3	US-08-906-616-171	Sequence 171, App
	25	13	65.0	537	3	US-08-639-075A-171	Sequence 171, App
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	28	13	65.0	537	4	US-08-906-613-171	Sequence 171, App
	29	13	65.0	1938	4	US-09-232-200-29	Sequence 29, Appl
	30	13	65.0	1938	4	US-09-232-197-29	Sequence 29, Appl
	31	13	65.0	1938	4	US-09-232-201-29	Sequence 29, Appl
c	32	13	65.0	3000	2	US-08-896-344A-1	Sequence 1, Appli
c	33	13	65.0	3000	4	US-09-360-682A-1	Sequence 1, Appli
	34	13	65.0	3217	4	US-09-232-200-64	Sequence 64, Appl
	35	13	65.0	3217	4	US-09-232-197-64	Sequence 64, Appl
	36	13	65.0	3217	4	US-09-232-201-64	Sequence 64, Appl
c	37	13	65.0	4403765	4	US-09-103-840A-2	Sequence 2, Appli
	38	12	60.0	391	1	US-08-636-928-6	Sequence 6, Appli
	39	12	60.0	412	4	US-08-976-259-123	Sequence 123, App
c	40	12	60.0	645	1	US-08-459-586-19	Sequence 19, Appl
c	41	12	60.0	645	2	US-08-282-696-19	Sequence 19, Appl
	42	12	60.0	648	5	PCT-US96-04648-4	Sequence 4, Appli
c	43	12	60.0	709	1	US-08-459-586-20	Sequence 20, Appl
c	44	12	60.0	709	2	US-08-282-696-20	Sequence 20, Appl
c	45	12	60.0	728	4	US-08-998-416-615	Sequence 615, App

ALIGNMENTS

RESULT 1
US-08-313-185-59/c
; Sequence 59, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-59

Query Match 100.0%; Score 20; DB 2; Length 432;

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  Best Local Similarity   100.0%;  Pred. No. 0.00054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
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Db    428 TACGGCGTTTCGATGAACCC 409


RESULT   2
US-09-082-614A-59/c
; Sequence 59, Application US/09082614A
; Patent No. 6124098
;  GENERAL INFORMATION:
;    APPLICANT:  Heym, Beate
;    APPLICANT:  Cole, Stewart
;    APPLICANT:  Young, Douglas
;    APPLICANT:  Zhang, Ying
;    APPLICANT:  Honore, Nadine
;    APPLICANT:  Telenti, Amalio
;    APPLICANT:  Bodmer, Thomas
;    TITLE OF INVENTION:  Rapid Detection of Antibiotic Resistance
;    TITLE OF INVENTION:  in Mycobacterium Tuberculosis
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/082,614A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/313,185
;      FILING DATE:  12-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  02356.0068-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-082-614A-59


  Query Match           100.0%;  Score 20;  DB 3;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 0.00054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
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Db    428 TACGGCGTTTCGATGAACCC 409


RESULT   3
US-08-757-653-135/c
; Sequence 135, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/757,653
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  FORS-02565
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  135:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  620 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-757-653-135


  Query Match           100.0%;  Score 20;  DB 2;  Length 620;
  Best Local Similarity   100.0%;  Pred. No. 0.00054;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tacggcgtttcgatgaaccc 20
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Db    296 TACGGCGTTTCGATGAACCC 277


RESULT   4
US-08-757-653-136/c
; Sequence 136, Application US/08757653
; Patent No. 5843669
;  GENERAL INFORMATION:
;    APPLICANT:  Kaiser, Michael W.
;    APPLICANT:  Lyamichev, Victor I.
;    APPLICANT:  Lyamichev, Natasha
;    TITLE OF INVENTION:  Cleavage Of Nucleic Acid Using
;    TITLE OF INVENTION:  Thermostable FEN-1 Endonucleases
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
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